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OM protein - protein search, using sw model

Run on: January 11, 2006, 15:07:51 ; Search time 77 Seconds
(without alignments)
992.882 Million cell updates/sec

Title: US-10-650-123-2
Perfect score: 868
Sequence: 1 MKKALATIALPALPAALAE.....VNTKVRSGELSGVRVKF 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003s.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	100.0	174	2 AAW04891	Aaw04891 Proteinase
2	868	100.0	174	6 ABU79079	Abu79079 N. mening
3	868	100.0	174	7 ADF43316	Adf43316 N. mening
4	868	100.0	174	8 ADL16114	Adl16114 Neisseria
5	868	100.0	174	8 ADL13428	Adl13428 Neisseria
6	868	100.0	174	8 ADL24352	Adl24352 N. meningi
7	868	100.0	174	9 AEA03010	Aea03010 Neisseria
8	864	99.5	174	9 AEP08236	Aep08236 Neisseria
9	864	99.5	174	9 AEB93444	Aeb93444 Neisseria
10	857	98.7	174	8 ADL24383	Adl24383 N. meningi
11	854	98.4	174	2 AAW04893	Aaw04893 Proteinase
12	825	95.0	174	2 AAW04894	Aaw04894 Proteinase
13	825	95.0	174	5 ABG91063	Abg91063 Neisseria
14	824.5	95.0	175	2 AAW04892	Aaw04892 Proteinase
15	820	94.5	166	8 ADL24385	Adl24385 N. meningi
16	809.5	93.3	175	6 ABP77991	Abp77991 N. gonorr
17	794	91.5	162	8 ADL24387	Adl24387 N. meningi
18	793	91.4	162	8 ADL24386	Adl24386 N. meningi
19	785	90.4	155	4 AAB19895	Aab19895 Neisseria
20	781	90.0	155	8 ADL13426	Adl13426 Neisseria
21	779.5	89.8	161	8 ADL24384	Adl24384 N. meningi
22	746	85.9	154	8 ADL24388	Adl24388 N. meningi
23	657.5	75.7	141	8 ADL24389	Adl24389 N. meningi
24	234	27.0	208	5 AAO17579	Aao17579 M catarrh

25	224	25.8	232	6	ABP79561	Abp79561 N. gonorr
26	221.5	25.5	176	5	AAU97605	Aau97605 Haemophil
27	221.5	25.5	176	5	AAU97603	Aau97603 Haemophil
28	221.5	25.5	176	5	AAU97602	Aau97602 Haemophil
29	221.5	25.5	176	5	AAU97604	Aau97604 Haemophil
30	218.5	25.2	229	6	ABP79854	Abp79854 N. gonorr
31	218	25.1	226	6	ABP79754	Abp79754 N. gonorr
32	214.5	24.7	176	5	AAU97601	Aau97601 Haemophil
33	214	24.7	281	6	ABP80738	Abp80738 N. gonorr
34	212	24.4	278	6	ABP80098	Abp80098 N. gonorr
35	210	24.2	265	6	ABP77624	Abp77624 N. gonorr
36	208	24.0	161	9	ABE91376	Aeb91376 Microbial
37	207.5	23.9	186	6	ABP80662	Abp80662 N. gonorr
38	206	23.7	241	9	ABE93440	Aeb93440 Neisseria
39	206	23.7	278	6	ABP80428	Abp80428 N. gonorr
40	204.5	23.6	229	6	ABP77612	Abp77612 N. gonorr
41	194.5	22.4	227	6	ABP77150	Abp77150 N. gonorr
42	194.5	22.4	227	6	ABP76762	Abp76762 N. gonorr
43	178	20.5	189	6	ABP78327	Abp78327 N. gonorr
44	141	16.2	27	8	ADL27222	Adl27222 Peptide f
45	141	16.2	27	9	ABE87498	Aeb87498 Neisseria

ALIGNMENTS

RESULT 1
AAW04891
ID AAW04891 standard; protein; 174 AA.
XX
AC AAW04891;
XX
DT 16-OCT-2003 (revised)
DT 22-DEC-1996 (first entry)
XX
DE Proteinase K resistant N. meningitidis 22 kD surface protein.
XX
KW Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;
KW antibody; detection; probe; surface protein.
XX
OS Neisseria meningitidis; strain 608B.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= sig_peptide 20..174
FT Protein /label= mat_protein
XX
PN W03620442-AL
XX
PD 26-SEP-1996.
XX
PF 15-MAR-1996; 96MO-CA000157.
XX
PR 17-MAR-1995; 95US-00406362.
PR 04-AUG-1995; 95US-0001983P.
XX
PA (IAPB-) IAP BIO VAC INC.
XX
PI Brodeur BR, Martin D, Hamel J, Rioux C;
XX
WI 1996-443187/44.
XX
DR N-PSDB; AAT39039.
XX
PT Neisseria meningitidis antigen, highly conserved between different
PT strains - useful for proddn. of antibodies for immunisation against, or
XX diagnosis of, N. meningitidis infection.
XX
PS Claim 7; Fig 1; 117pp; English.
XX
CC A proteinase K resistant surface protein has been isolated from 4 strains
CC of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,
CC antigenic fragments of antibodies can be used in a vaccine for the

1-6885-98

102/167

CC prevention of infection by N. meningitidis or by N. gonorrhoeae in
 CC humans. The antibodies may also be used diagnostically to detect N.
 CC meningitidis infection. The antigen may also be used to detect antibodies
 CC specific to N. meningitidis antigen. DNA sequences encoding the antigen,
 CC or their fragments, can be used as probes for the detection of pathogenic
 CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 174 AA;

Query Match 100.0%; Score 868; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
 QY 121 SQTSGIGLVLTGVSAYVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVKVF 174
 DB 121 SQTSGIGLVLTGVSAYVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVKVF 174

RESULT 2
 ABU79079
 ID ABU79079 standard; protein; 174 AA.
 XX
 AC ABU79079;
 DT 18-JUN-2003 (first entry)
 XX
 DE N. meningitidis lipopolysaccharide protein.
 XX
 KW Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
 KW gene therapy; mammalian cell receptor; cytostatic;
 KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;
 KW tumouricidal immunocyte; antitumour.
 XX
 OS Neisseria meningitidis.



XX US2002177551-A1.
 XX 28-NOV-2002.
 XX 30-MAY-2001; 2001US-00870759.
 XX 31-MAY-2000; 2000US-0208128P.
 XX (TERM/) Terman D S.
 XX Terman DS;
 XX
 XX WPI; 2003-361759/34.
 XX N-PSDB; ACA64711.
 XX
 XX A mammalian cell receptor, useful in the treatment of cancer by binding
 XX to tumor associated lipids where the binding induces anergy or apoptosis
 XX in T cells and antigen presenting cells.
 XX
 XX Disclosure; Page; 167pp; English.

XX The invention relates to a mammalian cell receptor, useful in the
 XX treatment of cancer, which binds to tumour associated lipids and induces
 XX anergy or apoptosis in the T cells and antigen presenting cells (APCs).
 XX Also included are a mammalian cell useful in the treatment of cancer
 XX where the receptor which binds tumour associated lipids and induces
 XX cellular inactivation or death is deleted or functionally deactivated,
 XX producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 XX (by allowing tumour associated lipids to contact immunocytes in which
 XX receptors for immunosuppressive fatty acids, ceramides, glycolipids,

CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 CC deleted), a construct useful in the treatment of cancer comprising a
 CC superantigen (Sag) nucleotide inserted into a virus, a mammalian T cell
 CC useful in the treatment of cancer (where an adaptor protein which
 CC inhibits T cell activation by tumour associated antigens is deleted or
 CC functionally deactivated), a composition useful in the treatment of
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 CC allowing tumour associated lipids to contact immunocytes, in which
 CC receptors for the lipids are inactivated or deleted to produce a
 CC tumouricidal immunocyte population, and administering the tumouricidal
 CC activated immunocytes to the host), producing (M3) a tumouricidal APC
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to
 CC contact APCs, in which receptors for the tumour associated lipids are
 CC inactivated or deleted to produce a tumouricidally activated population,
 CC and administering APCs to the host), producing a tumouricidal T cell
 CC population ex vivo in a mammal (by allowing a tumour associated lipids to
 CC contact T cells, in which adaptor proteins, which inhibit T cell
 CC activation by tumour associated antigens, are deleted or functionally
 CC deactivated to produce a tumouricidal population of T cells, and
 CC administering the tumouricidally activated T cells to the host, or
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
 CC administering the tumouricidally activated T cells to the host), treating
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a
 CC tumour associated antigen to contact immunocytes in which adaptor
 CC proteins which inhibit T cell activation by tumour associated antigens
 CC are deleted or functionally deactivated) and producing (M7) a
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 CC receptors, methods and compositions are useful for treating cancers and
 CC tumours. Bacterial superantigens are co-administered or administered as
 CC fusion constructs with anti-tumour proteins or motifs. The present
 CC sequence represents an anti-tumour protein which is co-administered with
 CC or incorporated into a fusion construct with a superantigen. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from the US patent
 CC office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"
 XX
 SQ Sequence 174 AA;

Query Match 100.0%; Score 868; DB 6; Length 174;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
 QY 121 SQTSGIGLVLTGVSAYVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVKVF 174
 DB 121 SQTSGIGLVLTGVSAYVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVKVF 174

RESULT 3
 ADF43316
 ID ADF43316 standard; protein; 174 AA.
 XX
 AC ADF43316;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DB N. meningitidis lipopolysaccharide seq id 36.
 XX
 KW receptor; lipid-based tumour associated antigen; cytostatic;
 KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
 KW infectious disease; lipopolysaccharide; LPS.

XX OS Neisseria meningitidis.
XX PN US2003157113-A1.
XX PD 21-AUG-2003.
XX PF 28-DEC-2000; 2000US-00751708.
XX PR 28-DEC-1999; 99US-0173371P.
XX PA (TERM/) Terman D S.
XX PI Terman DS;
XX DR WPI; 2003-787326/74.
XX DR N-PSDB; ADP43315.
XX XX
XX XX New receptor in a mammalian cell that inhibits regular activation by
XX PT receptors specific for lipid-based tumor associated antigens, useful for
XX PT treating a neoplastic disease or tumor, and infectious diseases.
XX XX
XX PS Disclosure; SEQ ID NO 36; 151pp; English.
XX CC The invention describes a receptor in a mammalian cell that inhibits
XX CC regular activation by receptors specific for lipid-based tumor
XX CC associated antigen. The receptor has cytostatic and antimicrobial
XX CC properties and is suitable for use in gene therapy. The receptors,
XX CC methods and compositions are useful for treating a neoplastic disease or
XX CC tumor (cancer), and infectious diseases. This is the amino acid sequence
XX CC of Neisseria meningitidis lipopolysaccharide (LPS) to which tumour cells
XX CC develop immunity.
XX SQ Sequence 174 AA;

Query Match 100.0%; Score 868; DB 7; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.1e-86;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120

QY 121 SQTSLGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174
Db 121 SQTSLGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174

RESULT 4
ADL16114
ID ADL16114 standard; protein; 174 AA.
AC ADL16114;
XX XX
XX XX 03-JUN-2004 (first entry)
XX DE Neisseria meningitidis NspA for use in vaccine.
XX KW Outer membrane vesicle preparation; OMV; detergent-free;
XX KW Physical disruption; vaccine; serogroup B; NspA;
XX KW Neisserial surface protein A; immunogen.
XX OS Neisseria meningitidis.
XX PN WO2004019977-A2.
XX PD 11-MAR-2004.
XX PF 01-SEP-2003; 2003WO-IB004293.

XX PR 30-AUG-2002; 2002GB-00020194.
XX PA (CHIR) CHIRON SRL.
XX PI Pizza M, Serruto D, Rappuoli R;
XX DR WPI; 2004-239124/22.
XX XX
XX XX Producing an outer membrane vesicle (OMV) preparation from a bacterium,
XX PT useful as a vaccine against Neisseria meningitidis serogroup B, comprises
XX PT disrupting the bacterial membrane in the absence of deoxycholate
XX PT detergent.
XX PS
XX PS Disclosure; Fig 3; 20pp; English.
XX CC The invention relates to a process for producing an outer membrane
XX CC vesicle (OMV) preparation from a bacterium. The process involves
XX CC disrupting the bacterial membrane substantially in the absence of
XX CC deoxycholate detergent or other detergent, followed by several
XX CC centrifugation steps. Membrane disruption is achieved by sonication,
XX CC homogenisation, microfluidisation, cavitation, osmotic shock, grinding,
XX CC French press, belnding or any other physical technique. The outer
XX CC membrane vesicles can be prepared from bacteria of the genera Moraxella,
XX CC Shigella, Pseudomonas, Treponema, Porphyromonas, Helicobacter or
XX CC Neisseria, and are particularly produced from Neisseria meningitidis
XX CC (especially serogroup B) or Neisseria gonorrhoeae. The invention also
XX CC relates to a Neisseria meningitidis outer membrane vesicle composition in
XX CC which the vesicles include the immunogens NspA (Neisserial surface
XX CC protein A; ADL16114), 287 protein (ADL16113) and 741 protein (ADL16112);
XX CC and the use of outer membrane vesicle compositions as a medicament,
XX CC especially for raising an immune response in a patient. The method is
XX CC useful for manufacturing an outer membrane vesicle preparation as a
XX CC vaccine against Neisseria meningitidis serogroup B. The present sequence
XX CC represents Neisseria meningitidis NspA.
XX SQ Sequence 174 AA;

Query Match 100.0%; Score 868; DB 8; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.1e-86;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120

QY 121 SQTSLGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174
Db 121 SQTSLGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174

RESULT 5
ADL13428
ID ADL13428 standard; protein; 174 AA.
XX XX
XX AC ADL13428;
XX XX
XX XX 03-JUN-2004 (first entry)
XX XX Neisseria meningitidis H44/76 full-length NspA protein.
XX DE Neisserial surface protein A; NspA; refolding; recombinant production;
XX KW vaccine; subunit vaccine; prevention; diagnosis; meningococcus;
XX KW invasive bacterial disease; bacteraemia; meningitis;
XX KW Neisseria gonorrhoeae; gonorrhoea; mature protein; strain H44/76;
XX KW antibacterial; gene therapy.
XX XX
XX OS Neisseria meningitidis; H44/76.
XX XX

FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein 20..174
 FT Misc-difference 168
 FT /label= Mature_NspA
 FT /note= "The corresponding residue in the mature protein
 shown in Fig 2 (residue 149) is Ala"
 XX WO2004020452-A2.
 XX 11-MAR-2004.
 XX 28-AUG-2003; 2003WO-EP010085.
 XX 30-AUG-2002; 2002GB-00020197.
 XX (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
 XX (UYUT-) RIJKSUNIV UTRECHT.
 XX Biemans R, Bos M, Denoel P, Feron C, Goraj K, Poolman J;
 XX Tommassen J, Weynants V;
 XX WPI; 2004-239150/22.
 XX N-PSDB; ADL13427.
 XX New refolded NspA protein, useful for preparing a composition for
 PT diagnosing, treating or preventing infection caused by Neisseria
 PT meningitidis or Neisseria gonorrhoeae.
 XX Disclosure; Fig 3; 62pp; English.
 XX The invention relates to an isolated refolded Neisserial surface protein
 CC A (NspA) from Neisseria meningitidis or Neisseria gonorrhoeae. The
 CC invention also relates to the method of refolding an NspA protein; an
 CC alkaline refolding buffer comprising ethanolamine and SB-12 (3-
 CC dimethyldecylammonopropanesulphonate) for refolding an NspA protein; a
 CC pharmaceutical composition comprising the refolded NspA protein, a
 CC carrier and optionally one or more other Neisserial antigens, a method of
 CC preventing or treating a Neisserial infection; an antibody immunospecific
 CC for the NspA protein; and diagnosing a Neisserial infection. NspA has
 CC characteristics which indicate that it is a potential vaccine candidate
 CC for the development of subunit vaccines for the treatment of infections
 CC caused by Neisseria meningitidis (meningococcus), which causes invasive
 CC bacterial diseases such as bacteraemia and meningitis, or Neisseria
 CC gonorrhoeae, the causative agent of gonorrhoea. Recombinantly produced
 CC NspA could therefore be used to produce vaccine compositions and it could
 CC also be used in the development of new antimicrobial agents, diagnostic
 CC tests and in drug screening. However, recombinantly produced proteins are
 CC frequently unable to adopt their biologically active conformations, and
 CC yields may be very low due to mis-folding and aggregation of the protein.
 CC The method of the invention provides an improved method for refolding the
 CC NspA protein, and it is possible to increase the recovery of active
 CC protein form partly purified inclusion bodies in amounts up to 100%
 CC without the need for further purification. The refolded NspA protein is
 CC useful for preparing a composition for diagnosing, treating or preventing
 CC infection caused by Neisseria meningitidis or Neisseria gonorrhoeae. The
 CC present sequence represents the full-length NspA protein from Neisseria
 CC meningitidis H44/76.
 XX SQ Sequence 174 AA;
 Query Match 100.0%; Score 868; DB 8; Length 174;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
 QY 121 SQTSGIGLVLTGVSAYATPNVDLDAGYRNYIGKVTNTKKNVRSGLSVGVVRVKF 174
 DB 121 SQTSGIGLVLTGVSAYATPNVDLDAGYRNYIGKVTNTKKNVRSGLSVGVVRVKF 174

QY 121 SQTSGIGLVLTGVSAYATPNVDLDAGYRNYIGKVTNTKKNVRSGLSVGVVRVKF 174
 DB 121 SQTSGIGLVLTGVSAYATPNVDLDAGYRNYIGKVTNTKKNVRSGLSVGVVRVKF 174
 RESULT 6
 ADL24352
 ID ADL24352 standard; protein; 174 AA.
 AC ADL24352;
 XX 03-JUN-2004 (first entry)
 XX N meningitidis strain 608B NspA protein.
 XX NspA; vaccine; antibacterial; meningitis.
 XX Neisseria meningitidis.
 XX WO2004019976-A2.
 XX 11-MAR-2004.
 XX 29-AUG-2003; 2003WO-CA001452.
 XX 30-AUG-2002; 2002US-0406980P.
 XX (SHIR-) SHIRE BIOCHEM INC.
 XX Martin D, Rioux S;
 XX WPI; 2004-239123/22.
 XX N-PSDB; ADL24351.
 XX Composition comprising liposome associated with isolated polypeptide or
 PT polynucleotide derived from Neisseria meningitidis strain 608B, or its
 PT fragment or analog, useful for inducing an immune response against N.
 PT meningitidis.
 XX Claim 1; Fig 1; 79pp; English.
 XX The present invention relates to a pharmaceutical composition comprising
 CC a liposome associated with an isolated polypeptide derived from Neisseria
 CC meningitidis strain 608B, where the polypeptide is the NspA protein. The
 CC composition is useful for inducing an immune response against N.
 CC meningitidis, for preventing and/or treating N. meningitidis infection
 CC and for treating and/or preventing neisserial infection chosen from N.
 CC meningitidis, N. gonorrhoeae, N. lactamica and N. polysaccharaea. It is
 CC useful for treatment or prophylaxis of meningitis and meningococemia, in
 CC a host. The host is a mammal, preferably a human and more preferably an
 CC adult human. The present sequence is the Neisseria meningitidis strain
 CC 608B NspA protein.
 XX SQ Sequence 174 AA;
 Query Match 100.0%; Score 868; DB 8; Length 174;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
 QY 121 SQTSGIGLVLTGVSAYATPNVDLDAGYRNYIGKVTNTKKNVRSGLSVGVVRVKF 174
 DB 121 SQTSGIGLVLTGVSAYATPNVDLDAGYRNYIGKVTNTKKNVRSGLSVGVVRVKF 174

RESULT 7
AEA03010
ID AEA03010 standard; protein; 174 AA.
XX
AC AEA03010;
XX
DT 28-JUL-2005 (first entry)
XX
DE Neisseria meningitidis meningococcal meningitis protein SEQ ID NO:36.
XX
KW tumor; neoplasm; gene therapy; immunotherapy; cytostatic; meningitis.
XX
OS Neisseria meningitidis.
XX
PN US2005112141-A1.
XX
RD 26-MAY-2005.
XX
PF 08-SEP-2004; 2004US-00937758.
XX
PR 30-AUG-2000; 2000US-00650884.
XX
PA (TERM/) Terman D S.
XX
PI Terman DS;
XX
DR WPI; 2005-394926/40.
XX
N-PSDB; AEA03009.
XX
PT New composition for treating a tumor or neoplastic disease in a subject
PT comprises conjugates comprising superantigen polypeptides or nucleic
PT acids with other molecules that produce a tumoricidal response.
XX
PS Disclosure; SEQ ID NO 36; 125pp; English.
XX
CC The invention relates to a composition for treating a tumor or neoplastic
CC disease in a subject. Also described: (1) a mammalian cell comprising an
CC exogenous nucleic acid encoding a superantigen expressed in the cell,
CC which cell also produces or expresses all alpha-anomers of
CC monoglycosylceramide or diglycosylceramide, where expression of the
CC superantigen and the mono- or diglycosylceramide is capable of eliciting
CC an antitumor immune response in a mammal into which the cell is
CC introduced; (2) treating a tumor or neoplastic disease in a subject; (3)
CC preparing a population of immunotherapeutic T or natural killer T (NK)T
CC cells useful to treat a tumor or neoplastic disease in a subject; (4) an
CC apoptotic cell preparation or lysate useful for treating a tumor or
CC neoplastic disease in a subject, comprising a cell population that has
CC been transfected with naked DNA encoding a superantigen, and treated to
CC undergo apoptosis or lysis; and (5) a cell that has ingested or been
CC transfected with the above apoptotic preparation or lysate, thus,
CC rendering the cell effective in presenting material expressed from
CC transfecting nucleic acid or material ingested to the immune system of a
CC mammal to elicit an anti-tumor immune response. The composition and
CC methods are useful for treating tumors or neoplastic diseases. The
CC present sequence represents a Neisseria meningitidis protein sequence
CC which induces meningococcal meningitis, which is given in the
CC exemplification of the present invention. Note - The sequence data for
CC this patent is not represented in the printed specification, but was
CC obtained in electronic format directly from the USPTO web site.
XX
SQ Sequence 174 AA;
Query Match 100.0%; Score 868; DB 9; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.1e-86;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120
Db 61 FAVDYTRYKNKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120

QY 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRYNYIGKVTYKVRSGELSVGVRYKF 174
Db 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRYNYIGKVTYKVRSGELSVGVRYKF 174
RESULT 8
ADP08236
ID ADP08236 standard; protein; 174 AA.
XX
AC ADP08236;
XX
DT 26-AUG-2004 (first entry)
XX
DE Neisseria meningitidis MC58 OMV-related membrane protein - SEQ ID 69.
XX
KW outer-membrane vesicle; antibacterial; antiinflammatory;
KW meningococcal protein trafficking; localisation; infection; vaccine;
KW gene therapy.
XX
OS Neisseria meningitidis MC58.
XX
PN WO2004046127-A2.
XX
PD 03-JUN-2004.
XX
PF 17-NOV-2003; 2003WO-IB006281.
XX
PR 15-NOV-2002; 2002GB-00026734.
XX
PR 27-MAR-2003; 2003GB-00007131.
XX
PA (CHIR) CHIRON SRL.
XX
PI Norais N, Grandi G;
XX
DR WPI; 2004-420615/39.
XX
PT New compositions having outer-membrane vesicles and proteins from
PT Neisseria meningitidis, useful in the field of meningococcal
PT biochemistry, in particular for preventing and/or treating meningococcal
PT infections.
XX
PS Claim 9; SEQ ID NO 69; 79pp; English.
XX
CC The invention relates to a novel composition comprising outer-membrane
CC vesicles (OMV) prepared from a first strain of Neisseria meningitidis and
CC 1 or more proteins which are present in OMVs prepared from a second
CC strain of N. meningitidis, but which are not present in OMVs prepared
CC from the first strain. The composition of the invention demonstrates
CC antibacterial and antiinflammatory activities and may be useful in the
CC field of meningococcal biochemistry, in particular the trafficking and
CC localisation of meningococcal proteins, as well as in the prevention or
CC treatment of meningococcal infections, possibly via the production of a
CC vaccine or gene therapy. The current sequence is that of a Neisseria
CC meningitidis MC58 outer-membrane vesicle (OMV)-related membrane protein
CC of the invention.
XX
SQ Sequence 174 AA;
Query Match 99.5%; Score 864; DB 8; Length 174;
Best Local Similarity 99.4%; Pred. No. 2.9e-86;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120
Db 61 FAVDYTRYKNKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120
QY 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRYNYIGKVTYKVRSGELSVGVRYKF 174
Db 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRYNYIGKVTYKVRSGELSVGVRYKF 174

CC and the wild-type NepA protein shown in Figure 1.

XX SQ Sequence 174 AA;
Query Match 98.7%; Score 857; DB 8; Length 174;
Best Local Similarity 98.9%; Pred. No. 1.7e-85;
Matches 172; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSP 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSP 120
Qy 121 SQTSGIGLVLTGVSVAVTNPVNDLDAGYRNYIGKVTNKVNRSGELSGVGRVKF 174
Db 121 SQTSGIGLVLTGVSVAVTNPVNDLDAGYRNYIGKVTNKVNRSGELSGVGRVKF 174

RESULT 11

AAW04893
ID AAW04893 standard; protein; 174 AA.
XX AC AAW04893;
XX AC
DT 16-OCT-2003 (revised)
DT 22-DEC-1996 (first entry)
XX
DE Proteinase K resistant N. meningitidis 22 kD surface protein.
XX
XX Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;
KW antibody; detection; probe; surface protein.
XX
XX Neisseria meningitidis; strain Z4063.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= sig_peptide
FT Protein 20..174
FT /label= mat_protein
XX
XX WO9629412-A1.
XX
XX 26-SEP-1996.
XX
XX 15-MAR-1996; 96WO-CA000157.
XX
XX 17-MAR-1995; 95US-00406362.
PR 04-AUG-1995; 95US-0001983P.
XX
XX (IAPB-) IAP BIO VAC INC.

XX Brodeur BR, Martin D, Hamel J, Rioux C;
XX WPI; 1996-443187/44.
XX N-PSDB; AAT39041.
XX
XX Neisseria meningitidis antigen, highly conserved between different
PT strains - useful for prodn. of antibodies for immunisation against, or
PT diagnosis of, N. meningitidis infection.
XX
XX Claim 7; Fig 9; 117pp; English.

XX A proteinase K resistant surface protein has been isolated from 4 strains
CC of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,
CC antigenic fragments of antibodies can be used in a vaccine for the
CC prevention of infection by N. meningitidis or by N. gonorrhoeae in
CC humans. The antibodies may also be used diagnostically to detect N.
CC meningitidis infection. The antigen may also be used to detect antibodies
CC specific to N. meningitidis antigen. DNA sequences encoding the antigen,
CC or their fragments, can be used as probes for the detection of pathogenic

CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
XX SQ Sequence 174 AA;

Query Match 98.4%; Score 854; DB 2; Length 174;
Best Local Similarity 98.3%; Pred. No. 3.7e-85;
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSP 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSP 120
Qy 121 SQTSGIGLVLTGVSVAVTNPVNDLDAGYRNYIGKVTNKVNRSGELSGVGRVKF 174
Db 121 SQTSGIGLVLTGVSVAVTNPVNDLDAGYRNYIGKVTNKVNRSGELSGVGRVKF 174

RESULT 12

AAW04894
ID AAW04894 standard; protein; 174 AA.
XX AC AAW04894;
XX AC
DT 16-OCT-2003 (revised)
DT 22-DEC-1996 (first entry)
XX
DE Proteinase K resistant N. meningitidis 22 kD surface protein.
XX
XX Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;
KW antibody; detection; probe; surface protein.
XX
XX Neisseria meningitidis; strain b2.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= sig_peptide
FT Protein 20..174
FT /label= mat_protein
XX
XX WO9629412-A1.
XX
XX 26-SEP-1996.
XX
XX 15-MAR-1996; 96WO-CA000157.
XX
XX 17-MAR-1995; 95US-00406362.
PR 04-AUG-1995; 95US-0001983P.
XX
XX (IAPB-) IAP BIO VAC INC.

XX Brodeur BR, Martin D, Hamel J, Rioux C;
XX WPI; 1996-443187/44.
XX N-PSDB; AAT39042.

XX Neisseria meningitidis antigen, highly conserved between different
PT strains - useful for prodn. of antibodies for immunisation against, or
PT diagnosis of, N. meningitidis infection.
XX
XX Claim 7; Fig 10; 117pp; English.

XX A proteinase K resistant surface protein has been isolated from 4 strains
CC of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,
CC antigenic fragments of antibodies can be used in a vaccine for the
CC prevention of infection by N. meningitidis or by N. gonorrhoeae in
CC humans. The antibodies may also be used diagnostically to detect N.
CC meningitidis infection. The antigen may also be used to detect antibodies
CC specific to N. meningitidis antigen. DNA sequences encoding the antigen,
CC or their fragments, can be used as probes for the detection of pathogenic

```

CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 174 AA;

Query Match 95.0%; Score 825; DB 2; Length 174;
Best Local Similarity 94.3%; Pred. No. 5.6e-82;
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGSDSF 120

Qy 121 SQTSGIGLVLTGVSAYATPNVDLDAGYRNYIGKVTNKVNRSGELSVGVVRVKF 174
Db 121 SKTSAGLGLVLAGVSAYATPNVDLDAGYRNYVGKVTNKVNRSGELSVGVVRVKF 174

RESULT 13
ABG91063
ID ABG91063 standard; protein; 174 AA.
XX
AC ABG91063;
XX
DT 29-NOV-2002 (first entry)
XX
DE Neisseria gonorrhoeae outer membrane protein #1.
XX
KW Gram-negative bacterial bleb; PorB; outer membrane protein;
KW Chlamydia trachomatis infection; Chlamydia pneumoniae infection;
KW protective antigen; antibacterial; vaccine.
XX
OS Neisseria gonorrhoeae.
XX
PN WO200262380-A2.
XX
PD 15-AUG-2002.
XX
PF 08-FEB-2002; 2002WO-EP001356.
XX
PR 08-FEB-2001; 2001GB-00003169.
XX
PA (SMIK ) SMITHLINE BEECHAM BIOLOGICALS.
XX
PI Berthet FJ, Lobet Y, Poolman J, Verlant VGCL;
XX
WPI; 2002-657510/70.
XX
N-PSDB; ABS67381.
XX
Novel gram-negative bacterial bleb presenting on its surface PorB outer
PT membrane protein from Chlamydia trachomatis or protective antigen from
PT Chlamydia pneumoniae, useful for preventing Chlamydia infection.
XX
PS Disclosure; Page 54; 75pp; English.
XX
The present invention relates to a new gram-negative bacterial bleb
CC presenting on its surface the PorB outer membrane protein from Chlamydia
CC trachomatis, or a protective antigen from C. pneumoniae. The invention is
CC useful for preventing C. trachomatis or C. pneumoniae infection in a
CC host. The present amino acid sequence represents a Neisseria gonorrhoeae
CC protein as described in the invention
XX
SQ Sequence 174 AA;

Query Match 95.0%; Score 825; DB 5; Length 174;
Best Local Similarity 94.3%; Pred. No. 5.6e-82;
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGSDSF 120

Qy 121 SQTSGIGLVLTGVSAYATPNVDLDAGYRNYIGKVTNKVNRSGELSVGVVRVKF 174
Db 121 SKTSAGLGLVLAGVSAYATPNVDLDAGYRNYVGKVTNKVNRSGELSVGVVRVKF 174

RESULT 14
AAW04892
ID AAW04892 standard; protein; 175 AA.
XX
AC AAW04892;
XX
DT 16-OCT-2003 (revised)
DT 22-DEC-1996 (first entry)
XX
DE Proteinase K resistant N. meningitidis 22 kD surface protein.
XX
KW Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;
KW antibody; detection; probe; surface protein.
XX
OS Neisseria meningitidis; strain MCH88.
XX
PH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= sig_peptide
FT Protein /label= mat_protein
XX
PN WO9629412-A1.
XX
PD 26-SEP-1996.
XX
PF 15-MAR-1996; 96WO-CA000157.
XX
PR 17-MAR-1995; 95US-00406362.
XX
PR 04-AUG-1995; 95US-0001983P.
XX
PA (IAFB-) IAF BIO VAC INC.
XX
PI Brodeur BR, Martin D, Hamel J, Rioux C;
XX
WPI; 1996-443187/44.
XX
N-PSDB; AAT39040.
XX
Neisseria meningitidis antigen, highly conserved between different
PT strains - useful for prodn. of antibodies for immunisation against, or
PT diagnosis of, N. meningitidis infection.
XX
Claim 7; Fig 8; 117pp; English.
XX
A proteinase K resistant surface protein has been isolated from 4 strains
CC of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,
CC antigenic fragments of antibodies can be used in a vaccine for the
CC prevention of infection by N. meningitidis or by N. gonorrhoeae in
CC humans. The antibodies may also be used diagnostically to detect N.
CC meningitidis infection. The antigen may also be used to detect antibodies
CC specific to N. meningitidis antigen. DNA sequences encoding the antigen,
CC or their fragments, can be used as probes for the detection of pathogenic
CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 175 AA;

Query Match 95.0%; Score 824.5; DB 2; Length 175;
Best Local Similarity 95.4%; Pred. No. 6.4e-82;
Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

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Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDS 119
Db 61 FAVDYTRYKNYKQVSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDS 120
QY 120 FSQTSIGLGLTGVSYAVTPNVDLDAGYRYNYIGKNTVKNVRSGLSVGVVKF 174
Db 121 FSQTSIGLGLAGVSYAVTPNVDLDAGYRYNYIGKNTVKNVRSGLSVGVVKF 175

RESULT 15
ADL24385
ID ADL24385 standard; protein; 166 AA.
XX AC ADL24385;
XX 03-JUN-2004 (first entry)
XX DE N meningitidis strain 608B modified NspA protein #3.
XX KW mutein; mutant; NspA; vaccine; antibacterial; meningitis.
XX OS Neisseria meningitidis.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Misc-difference 35..36 /note= "wild-type NspA residues 36-43 deleted"
XX WO2004019976-A2.

XX 11-MAR-2004.
XX 29-AUG-2003; 2003WO-CA001452.
XX 30-AUG-2002; 2002US-0406980P.
XX (SHIR-) SHIRE BIOCHEM INC.
XX Martin D, Rioux S;
XX WPI; 2004-239123/22.
XX Composition comprising liposome associated with isolated polypeptide or
XX polynucleotide derived from Neisseria meningitidis strain 608B, or its
XX fragment or analog, useful for inducing an immune response against N.
XX meningitidis.

XX Example 4; Page; 79pp; English.
XX The present invention relates to a pharmaceutical composition comprising
XX a liposome associated with an isolated polypeptide derived from Neisseria
XX meningitidis strain 608B, where the polypeptide is the NspA protein. The
XX composition is useful for inducing an immune response against N.
XX meningitidis, for preventing and/or treating N. meningitidis infection
XX and for treating and/or preventing neisserial infection chosen from N.
XX meningitidis, N. gonorrhoeae, N. lactamica and N. polysaccharaea. It is
XX useful for treatment or prophylaxis of meningitis and meningococemia, in
XX a host. The host is a mammal, preferably a human and more preferably an
XX adult human. The present sequence is a modified version of the Neisseria
XX meningitidis strain 608B NspA protein. Note: This sequence is not shown
XX in the specification but has been created based on the information given
XX and the wild-type NspA protein shown in Figure 1.

XX Sequence 166 AA;
XX Query Match 94.5%; Score 820; DB 8; Length 166;
XX Best Local Similarity 95.4%; Pred. No. 1,8e-81;
XX Matches 166; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
|||||

Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAK-----KGFSPRISAGYRINDLR 52
QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120
Db 53 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 112
QY 121 SQTSGIGLGLTGVSYAVTPNVDLDAGYRYNYIGKNTVKNVRSGLSVGVVKF 174
Db 113 SQTSGIGLGLTGVSYAVTPNVDLDAGYRYNYIGKNTVKNVRSGLSVGVVKF 166

Search completed: January 11, 2006, 15:18:36
Job time : 79 secs

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OM protein - protein search, using sw model

Run on: January 11, 2006, 15:15:42 ; Search time 40 Seconds
(without alignments)
418.543 Million cell updates/sec

Title: US-10-650-123-2
Perfect score: 868
Sequence: 1 MKKALATLIALPALPAALAE.....VNTKVRSGELSGVGRVKF 174
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	864	99.5	174	2 G81174	outer membrane pro
2	854	98.4	174	2 B81932	outer membrane pro
3	244.5	28.2	261	2 S16610	opacity protein op
4	242	27.9	260	2 S16611	opacity protein op
5	241.5	27.8	338	2 S16613	opacity protein op
6	241	27.8	258	2 S16612	opacity protein op
7	241	27.8	260	1 KONH0	opacity protein op
8	240.5	27.7	237	2 S36343	opacity protein op
9	240.5	27.7	257	2 S16614	opacity protein op
10	239	27.5	266	2 S16616	opacity protein op
11	238	27.4	258	2 S08514	opacity protein-re
12	237	27.3	254	2 S20043	opacity protein B
13	237	27.3	270	2 S04380	opacity protein P.
14	236.5	27.2	268	1 KONH2C	opacity protein P.
15	236	27.2	283	2 S72343	opacity protein op
16	232.5	26.8	234	2 S36329	opacity protein op
17	232.5	26.8	282	2 S16617	opacity protein op
18	232	26.7	234	2 S36342	opacity protein op
19	232	26.7	234	2 S36341	opacity protein op
20	231	26.6	233	2 S36350	opacity protein op
21	226	26.0	234	1 KONH8	opacity protein V2
22	226	26.0	234	2 S36348	opacity protein op
23	226	26.0	238	2 S36349	opacity protein op
24	226	26.0	261	2 S16619	opacity protein op
25	224.5	25.9	243	2 S36346	opacity protein op
26	221	25.5	248	2 P10038	opacity protein D
27	219	25.2	238	2 S36344	opacity protein ho
28	217	25.0	178	2 F64124	opacity protein ho
29	215	24.8	239	2 S28630	opacity protein op

30	205.5	23.7	247	2 S28627	opacity protein op
31	203.5	23.4	214	2 S44706	opacity protein op
32	189.5	21.8	235	2 S44707	opacity protein op
33	180	20.7	121	2 I64187	opacity protein ho
34	150.5	17.3	210	2 S77737	opacity protein op
35	141	16.2	187	2 S20044	opacity protein op
36	135	15.6	168	2 S08513	opacity protein-re
37	135	15.6	170	2 T10256	opacity protein-re
38	132	15.2	239	2 AH0541	probable outer mem
39	129.5	14.9	281	2 AH3012	outer surface prot
40	129.5	14.9	284	2 G98271	hypothetical prote
41	126.5	14.6	70	2 F64086	probable outer mem
42	126.5	14.6	201	2 S16286	opacity protein op
43	126	14.5	192	2 S44712	opacity protein op
44	122	14.1	284	2 AG3556	heat resistant agg
45	121.5	14.0	264	2 I54668	heat resistant agg

ALIGNMENTS

RESULT 1

G81174
outer membrane protein NsgA NMB0663 [imported] - Neisseria meningitidis (strain MC58 ser C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: G81174
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; R. B. Jin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, C., Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: G81174
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-174 <TET>
A;Cross-references: UNIPROT:Q9RP17; UNIPARC:UPI000000D41C1; GB:AE002420; GB:AE002098; NID A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0663

Query Match 99.5%; Score 864; DB 2; Length 174;
Best Local Similarity 99.4%; Pred. No. 6.9e-70;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR	60
Db	1	MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR	60
Qy	61	FADVTRYKNYKAPSTDFKLYSIGASALYDFTQSPVKPYLGARLSLNRSVDLGGDSF	120
Db	61	FADVTRYKNYKAPSTDFKLYSIGASALYDFTQSPVKPYLGARLSLNRSVDLGGDSF	120
Qy	121	SQTSIGLGLTGVSYAVTPNVLDLAGRYNYIGKVTNKVRSGLSGVGRVKF	174
Db	121	SQTSIGLGLTGVSYAVTPNVLDLAGRYNYIGKVTNKVRSGLSGVGRVKF	174

RESULT 2

B81932
outer membrane protein NMA0862 [imported] - Neisseria meningitidis (strain Z2491 serogroup C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: B81932
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491. A;Reference number: AB1775; MUID:20222556; PMID:10761919
A;Accession: B81932
A;Status: preliminary

```
A:Molecule type: DNA
A:Residues: 1-174 <PAR>
A:Cross-references: UNIPROT:P95372; UNIPARC:UPI00000D41C0; GB:AL1162754; GB:AL1157959; NID
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: nspA; NMA0862

Query Match      98.4%; Score 854; DB 2; Length 174;
Best Local Similarity 98.3%; Pred. No. 5.4e-69;
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPTDPKLYSIGASALYDPTQSPVKPYLGARLSNRAVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPTDPKLYSIGASALYDPTQSPVKPYLGARLSNRAVDLGGSDSF 120

Qy 121 SQTSLGLVLTGVSAYVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 174
Db 121 SQTSLGLVLTGVSAYVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 174

RESULT 3
S16610
opacity protein opaK precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
N:Alternate names: outer membrane protein opaK
C:Species: Neisseria gonorrhoeae
A:Variety: strain MS11
C:Date: 13-Jan-1995 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C:Accession: S16610
R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch,
Mol. Microbiol. 5, 1989-1901, 1991
A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fami
A:Reference number: S16610; MUID:92114767; PMID:1815562
A:Accession: S16610
A:Molecule type: DNA
A:Residues: 1-261 <BHA>
A:Cross-references: UNIPARC:UPI0000178215; EMBL:X52364
A:Experimental source: strain MS11, variant 4.8
A:Note: the authors did not translate the sequence for the signal peptide
A:Note: expression of opacity proteins is regulated by the number of translated repeat e
of repeats place the start codon in frame with the rest of the protein
C:Genetics:
A:Gene: opaK
C:Superfamily: opacity protein
C:Keywords: cell surface component; transmembrane protein
F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
F:24-261/Product: opacity protein opaK #status predicted <MAT>
F:34-42/Domain: transmembrane #status predicted <TM1>
F:43-75/Domain: extracellular #status predicted <EXT1>
F:51-61/Region: semivariable region
F:76-84/Domain: transmembrane #status predicted <TM2>
F:89-95/Domain: transmembrane #status predicted <TM3>
F:96-134/Domain: extracellular #status predicted <EXT2>
F:102-129/Region: hypervariable region HV1
F:135-149/Domain: transmembrane #status predicted <TM4>
F:155-165/Domain: transmembrane #status predicted <TM5>
F:166-212/Domain: extracellular #status predicted <EXT3>
F:171-218/Region: hypervariable region HV2
F:213-225/Domain: transmembrane #status predicted <TM6>
F:229-237/Domain: transmembrane #status predicted <TM7>
F:238-252/Domain: extracellular #status predicted <EXT4>
F:253-261/Domain: transmembrane #status predicted <TM8>

Query Match      28.2%; Score 244.5; DB 2; Length 261;
Best Local Similarity 29.9%; Pred. No. 1.9e-14;
Matches 73; Conservative 26; Mismatches 59; Indels 87; Gaps 10;

Qy 15 AAALAEAG-ASGFTYQADAAHAKA-----SSLSGSAKG-----FSPRI 50
Db 21 AQAASEGNRGPYQADALAYAAERITHDYPTGAKGKTTISTVSDYFRNIRTHSIHPRV 80
```

```
Qy 51 SAGYRINDLRFAVDYTRYKNY-----KAPSTDFK-----LYS 82
Db 81 SVGVDFGWMRIADARYARKNNKYSVSIKELLRNKNGNRITDLKAENQENGTFHAVSS 140

Qy 83 IGASAIYDFTQSPVKPYLGARLSN--RASVD-----LGG----- 116
Db 141 LGLSAVYDFKLNDFKFPYIGARVAYGHVRSIDSTKTKTEVTTLHGFGTTPTVYPGKNT 200

Qy 117 -----SDFSQTSIGGLVLTGVSAYVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGV 170
Db 201 QNAHRESDSIRR--VGLGAVAGVGDITPNLTLDAGYRYHWGRLENTF-KTHEASLGV 257

Qy 171 RVKF 174
Db 258 RYRP 261

RESULT 4
S16611
opacity protein opaJ precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
N:Alternate names: outer membrane protein opa58
C:Species: Neisseria gonorrhoeae
A:Variety: strain MS11
C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C:Accession: S16611; S36345; S28624
R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch,
Mol. Microbiol. 5, 1989-1901, 1991
A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fami
A:Reference number: S16610; MUID:92114767; PMID:1815562
A:Accession: S16611
A:Molecule type: DNA
A:Residues: 1-260 <BHA>
A:Cross-references: UNIPROT:Q04882; UNIPARC:UPI00001781FE; EMBL:X52371
A:Experimental source: strain MS11, variant 4.8
A:Note: the authors did not translate the sequence for the signal peptide
A:Note: expression of opacity proteins is regulated by the number of translated repeat e
of repeats place the start codon in frame with the rest of the protein
R:Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
EMBO J. 12, 641-650, 1993
A:Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms di
A:Reference number: S36328; MUID:93178439; PMID:8440254
A:Accession: S36345
A:Molecule type: DNA
A:Residues: 24-260 <KUP>
A:Cross-references: UNIPARC:UPI0000130D60; EMBL:Z18937; NID:G49333; PIDN:CAA79370.1; PID
A:Experimental source: strain MS11, variant F3
A:Note: expression of opacity proteins is regulated by the number of translated repeat e
of repeats place the start codon in frame with the rest of the protein
C:Genetics:
A:Gene: opaJ
C:Superfamily: opacity protein
C:Keywords: cell surface component; transmembrane protein
F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
F:24-260/Product: opacity protein opaJ #status predicted <MAT>
F:34-42/Domain: transmembrane #status predicted <TM1>
F:43-74/Domain: extracellular #status predicted <EXT1>
F:51-60/Region: semivariable region
F:75-83/Domain: transmembrane #status predicted <TM2>
F:88-94/Domain: transmembrane #status predicted <TM3>
F:95-133/Domain: extracellular #status predicted <EXT2>
F:101-128/Region: hypervariable region HV1
F:134-148/Domain: transmembrane #status predicted <TM4>
F:154-164/Domain: transmembrane #status predicted <TM5>
F:165-211/Domain: extracellular #status predicted <EXT3>
F:170-217/Region: hypervariable region HV2
F:212-224/Domain: transmembrane #status predicted <TM6>
F:228-236/Domain: transmembrane #status predicted <TM7>
F:237-251/Domain: extracellular #status predicted <EXT4>
F:252-260/Domain: transmembrane #status predicted <TM8>

Query Match      27.9%; Score 242; DB 2; Length 260;
Best Local Similarity 29.5%; Pred. No. 3.2e-14;
```


F;212-224/Domain: transmembrane #status predicted <TM6>
F;228-236/Domain: transmembrane #status predicted <TM7>
F;237-251/Domain: extracellular #status predicted <EXT4>
F;252-260/Domain: transmembrane #status predicted <TM6>

```

Query Match          27.8%; Score 241; DB 1; Length 260;
Best Local Similarity 28.8%; Pred.No. 4e-14;
Matches 72; Conservative 30; Mismatches 64; Indels 84; Gaps 9;

QY      6 ATLIATLAPAAALAEAGSGFYVQADAAHA-----KASSSLGSAKGFS----- 47
       ::::   :::::  |||:|||||:|
Db      14 SLLFFSAAQAASEDCGRGFYVQADLAYAVEHITHDYPKPTDPSKGKISTVSDFYRNRT 73
       ::::   :::::  |||:|||||:|

QY      48 -----PRISAGRYINDLRPAVDTRY-----KNYKAPSTD-- 77
       ||::|||:|||||:|||||:|
Db      74 HSHIPRVSYGDYFGWRIAADYARYRKWSDNKYSVSIKNMRVHKHSNRKRLKTENOENG 133
       ||::|||:|||||:|||||:|

QY      78 --FKLYSIGASAIYDFDTQSPVKPYGLCARLSN--RASVD-----LGG- 116
       ::::   :::::  |||:|||||:|
Db      134 SFHAVSSLGSAIYDFQINDKFPYIGARVAYGHVRHSIDSTKKITGLTTTTPGIMSGV 193
       ::::   :::::  |||:|||||:|

QY      117 -----SDSPSQTSIGLGVLTVGSYAVTPNVDDLDAGYRNYIGKVNTVTKVNRVG 164
       |||:   ||::|||:|||||:|
Db      194 YKVLRTPGAHRSDSIR--VGLGIAGVGFDITPKLTLDAGYRYHNWGLEINTR-FKTH 250
       |||:   ||::|||:|||||:|

QY      165 ELSGVGRVKF 174
       ||::|||:|
Db      251 EASLGVRVRF 260
       ||::|||:|
```

RESULT 8

S36343
opacity protein opa57 - Neisseria gonorrhoeae (strain MS11) (fragment)
N;Alternate names: outer membrane protein opa57
C;Species: Neisseria gonorrhoeae
A;Variety: strain MS11
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S36343; S28626
R;Kupsch, B.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
EMBO J. 12. 641-650. 1993
A;Title: Variable opacity (Opa) outer membrane proteins account for the cell tr
A;Reference number: S36328; MUID:93178439; PMID:8440254
A;Accession: S36343
A;Molecule type: DNA
A;Residues: 1-237 <UP>
A;Cross-references: UNIPROT:Q04880; UNIPARC:UPI0000130D61; EMBL:Z18935; NID:g494
A;Experimental source: strain MS11, variant F3
A;Note: expression of opacity proteins is regulated by the number of translated
of repeats place the start codon in frame with the rest of the protein
C;Genetics:
A;Gene: opa57
C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;1-237/Product: opacity protein opa57 #status predicted <MAT>
F;11-19/Domain: transmembrane #status predicted <TM1>
F;20-51/Domain: extracellular #status predicted <EXT1>
F;28-37/Region: semivariable region
F;52-60/Domain: transmembrane #status predicted <TM2>
F;65-71/Domain: transmembrane #status predicted <TM3>
F;72-110/Domain: extracellular #status predicted <EXT2>
F;78-110/Region: hypervariable region HV1
F;111-125/Domain: transmembrane #status predicted <TM4>
F;131-141/Domain: transmembrane #status predicted <TM5>
F;142-188/Domain: extracellular #status predicted <EXT3>
F;147-194/Region: hypervariable region HV2
F;189-201/Domain: transmembrane #status predicted <TM6>
F;205-213/Domain: transmembrane #status predicted <TM7>
F;214-228/Domain: extracellular #status predicted <EXT4>
F;229-237/Domain: transmembrane #status predicted <TM8>

Query Match 27.7%; Score 240.5; DB 2; Length 237;
Best Local Similarity 29.6%; Pred.No. 3.9e-14;
Matches 71; **Conservative** 26; **Mismatches** 58; **Indels** 85; **Gaps** 9

R;Palmer, L.; Brooks, G.F.; Falkow, S.
Mol. Microbiol. 3, 663-671, 1989
A;Title: Expression of gonococcal protein II in *Escherichia coli* by translational fusion
A;Reference number: S04380; MUID:89343653; PMID:2503682
A;Accession: S04380
A;Molecule type: DNA
A;Residues: 1-270 <PAL>
A;Cross-references: UNIPROT:Q50959; UNIPARC:UPI000017821A; EMBL:X15780
A;Experimental source: strain F62-SF, serogroup IB-3; clone F62-SFG1
A;Note: the authors did not translate the sequence of the signal peptide
A;Note: expression of opacity proteins is regulated by the number of translated repeat
R;Tana, M.K.; So, M.; Seifert, H.S.; Billyard, E.; Marchal, C.
EMBO J. 7, 4367-4378, 1988
A;Title: Pilin expression in *Neisseria gonorrhoeae* is under both positive and negative
A;Reference number: S02017; MUID:89210824; PMID:2854063
A;Accession: S16504
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 259-270 <TAH>
A;Cross-references: UNIPARC:UPI00000AFOFB; EMBL:X13965
A;Experimental source: strain M311A
A;Note: expression of opacity proteins is regulated by the number of translated repeat
of repeats place the start codon in frame with the rest of the protein
C;Genetics:
A;Gene: opa1
C;Keywords: cell surface component; transmembrane protein
F;1-10/11-23/Domain: signal sequence (fragments) #status predicted <SIG>
F;24-270/Product: opacity protein opaK #status predicted <MAT>
F;34-42/Domain: transmembrane #status predicted <TM1>
F;43-75/Domain: extracellular #status predicted <EXT1>
F;51-61/Region: semivariable region
F;76-84/Domain: transmembrane #status predicted <TM2>
F;89-95/Domain: transmembrane #status predicted <TM3>
F;96-141/Domain: extracellular #status predicted <EXT2>
F;102-136/Region: hypervariable region HV1
F;142-156/Domain: transmembrane #status predicted <TM4>
F;162-172/Domain: transmembrane #status predicted <TM5>
F;173-221/Domain: extracellular #status predicted <EXT3>
F;178-227/Region: hypervariable region HV2
F;222-234/Domain: transmembrane #status predicted <TM6>
F;238-246/Domain: transmembrane #status predicted <TM7>
F;247-261/Domain: extracellular #status predicted <EXT4>
F;262-270/Domain: transmembrane #status predicted <TM8>

Query Match 27.3%; Score 237; DB 2; Length 270;
Best Local Similarity 27.1%; Pred. No. 9.4e-14;
Matches 72; Conservative 33; Mismatches 67; Indels 94; Gaps 8;
QY 2 KKALATLALPAALAEAG---ASGPFVQADAAH-----AKASSLSGSAK 44
DB 6 KKPSSLFSSLLPSSAAQAAGEGNGPGPVQADLAYAVEHITHDYPKPTGAKKGTITSVS 65
QY 45 GF-----SPRISAGYRINDLPAVDYTRYK----- 69
DB 66 DYFNIRTHSVHPRVSVGDFGFWRIAADYARYKNNKNYSIKELGRNDSASGVRG 125
QY 70 --NYKAPSTDFK-----LYSIGASAIYDFTQSPVKPYLGARLSL----- 107
DB 126 HLNITQKTEHQENGTFHAASLSGLSTIYDFTGSRFPKPYIGARVAYGHVRHQRVSVEQE 185
QY 108 -----NRASVDLGGSS-----DSFQSTQSIGLVLTGVSAVTPNVDLDAGYR 148
DB 186 TEIVTTPYKEQNVAPSPIPGAPTKKPAHBSRSISLFGAVAGVGIIDITNLTLDAGYR 245
QY 149 YNYIGKVNTPKVRSGELSVGVRVKF 174
DB 246 YHNWGLENTR-FKTHEASLGVRVRF 270

RESULT 14

KONH2C

opacity protein P.IIc precursor - *Neisseria gonorrhoeae* (strain JS3) (fragments)

N;Alternate names: outer membrane protein P.IIc
C;Species: *Neisseria gonorrhoeae*
A;Variety: strain JS3
C;Date: 31-Mar-1992 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C;Accession: S03095; S16360
R;van der Ley, P.
Mol. Microbiol. 2, 797-806, 1988
A;Title: Three copies of a single protein II-encoding sequence in the genome of *Neisseria*
A;Reference number: S03095; MUID:89096501; PMID:3145386
A;Accession: S03095
A;Molecule type: DNA
A;Residues: 1-268 <VAN>
A;Cross-references: UNIPROT:P09888; UNIPARC:UPI00001747E4; EMBL:X12625
A;Experimental source: strain JS3
A;Note: 241-Val was also found
A;Note: expression of opacity proteins is regulated by the number of translated repeat
of repeats place the start codon in frame with the rest of the protein
R;Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
Infect. Immun. 55, 2026-2031, 1987
A;Title: Antigenic and structural differences among six proteins II expressed by a single
A;Reference number: S16360; MUID:87306843; PMID:3114142
A;Accession: S16360
A;Status: preliminary
A;Molecule type: protein
A;Residues: 24-34 <BAR>
A;Cross-references: UNIPARC:UPI00001747E5
C;Genetics:
A;Gene: pilc
C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
F;24-268/Product: opacity protein P.IIc #status experimental <MAT>
F;34-42/Domain: transmembrane #status predicted <TM1>
F;43-74/Domain: extracellular #status predicted <EXT1>
F;51-60/Region: semivariable region
F;75-83/Domain: transmembrane #status predicted <TM2>
F;88-94/Domain: transmembrane #status predicted <TM3>
F;95-140/Domain: extracellular #status predicted <EXT2>
F;101-135/Region: hypervariable region HV1
F;141-155/Domain: transmembrane #status predicted <TM4>
F;161-171/Domain: transmembrane #status predicted <TM5>
F;172-219/Domain: extracellular #status predicted <EXT3>
F;177-225/Region: hypervariable region HV2
F;220-232/Domain: transmembrane #status predicted <TM6>
F;236-244/Domain: transmembrane #status predicted <TM7>
F;245-259/Domain: extracellular #status predicted <EXT4>
F;260-268/Domain: transmembrane #status predicted <TM8>

Query Match 27.2%; Score 236.5; DB 1; Length 268;
Best Local Similarity 26.8%; Pred. No. 1e-13;
Matches 69; Conservative 32; Mismatches 67; Indels 89; Gaps 8;
QY 6 ATLIALPALPAALAEAGSGFVQADAAHAKA-----SSSLSGSAK----- 44
DB 13 SSLIFSSAARAASDGGGPGPVQADLAYAERIHTDYPKPTGKKNKISTVSDYPRNIRT 72
QY 45 -GFSPRISAGYRINDLPAVDYTRYK-----NYKAPS 75
DB 73 HSHVHPRVSVGDFGFWRIAADYARYKNNKNYSIKELGRNDSASGVRGHLNIQTQK 132
QY 76 TDFK-----LYSIGASAIYDFTQSPVKPYLGARLSNRA-----SVDL----- 114
DB 133 TEHQENGTFHVASLSGLSTIYDFTGSRFPKPYIGARVAYGHVRHQRVSVEQETETITTPY 192
QY 115 ---CGSDSFSQ-----TSIGLVLTGVSAVTPNVDLDAGYRYNIGKVT 157
DB 193 SNGGKVSLSKMPKSAHQSNIRRVGLGVGIAGVGPDITPNLTLDGTGYRHNWGRLEN 252
QY 158 VKNVRSGELSVGVRVKF 174
DB 253 TR-FKTHEASLGVRVRF 268

RESULT 15

S72343
opacity protein opaH precursor - Neisseria gonorrhoeae (isolate 15063G)
N:Alternate names: cell invasion protein opaH
C:Species: Neisseria gonorrhoeae
A:Variety: isolate 15063G
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S72343
R:Waldbeser, L.S.; Ajioka, R.S.; Merz, A.J.; Puaoli, D.; Lin, L.; Thomas, M.; So, M.
Mol. Microbiol. 13, 919-928, 1994
A:Title: The opaH locus of Neisseria gonorrhoeae MS11A is involved in epithelial cell invasion
A:Reference number: S72343; MUID:95115561; PMID:7815949
A:Accession: S72343
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-283 <WAL>
A:Cross-references: UNIPROT:Q50943; UNIPARC:UPI00000BB96E; EMBL:U13708; NID:G535357; PID:15063G
A:Experimental source: isolate 15063G
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, August 1994
A:Note: expression of opacity proteins is regulated by the number of translated repeats of repeats place the start codon in frame with the rest of the protein
C:Superfamily: opacity protein
C:Keywords: cell surface component; transmembrane protein
F:1-48/Domain: signal sequence #status predicted <SIG>
F:49-283/Product: opacity protein opaH #status predicted <MAT>
F:58-66/Domain: transmembrane #status predicted <TM1>
F:67-98/Domain: extracellular #status predicted <EXT1>
F:75-84/Region: semivariable region
F:99-107/Domain: transmembrane #status predicted <TM2>
F:112-118/Domain: transmembrane #status predicted <TM3>
F:119-155/Domain: extracellular #status predicted <EXT2>
F:125-150/Region: hypervariable region HV1
F:156-170/Domain: transmembrane #status predicted <TM4>
F:176-186/Domain: transmembrane #status predicted <TM5>
F:187-234/Domain: extracellular #status predicted <EXT3>
F:192-240/Region: hypervariable region HV2
F:235-247/Domain: transmembrane #status predicted <TM6>
F:251-259/Domain: transmembrane #status predicted <TM7>
F:260-274/Domain: extracellular #status predicted <EXT4>
F:275-283/Domain: transmembrane #status predicted <TM8>

Query Match 27.2%; Score 236; DB 2; Length 283;

Best Local Similarity 27.9%; Pred. NO. 1.2e-13;

Matches 68; Conservative 29; Mismatches 67; Indels 80; Gaps 7;

Qy	10	ALALPAAALAEAGSGFYQDAAHAKA-----SSSLGSAGK-----FS 47
Db	41	SLLSAAQAASAMRGFYQDAFAAERITHDYPEPTGKKGITSTVSDYFRNIRTHSVH 100
Qy	48	PRISAGYRINDLRPAVDYTRYKNY-----KAPS-----TDFKLY 81
Db	101	PRVSVGYDFGGRWIRADYARKNNKYNKYNIRVQEAHNSRIDLKAENQENGTFHVS 160
Qy	82	SIGASAIYDFDTQSPKPYLGARLSN--RASVDL----- 114
Db	161	SLGLSAVYDFPKLNDKFKYIGARVAYGHVRHSIDSTKTKILTSFYGVATKPTTYDIGP 220
Qy	115	-----GGSDSFQTSIGLGLTGVSVAVTPNVVDLAGRYNYIKVNTVKNVRSGLSVGV 170
Db	221	KTQDAHQESNSIRRVGLGVAGVGPDTPKLTDTGYRYHWRLENTN-FKTHEASLGM 279
Qy	171	RVKF 174
Db	280	RYRP 283

Search completed: January 11, 2006, 15:22:19

Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 11, 2006, 15:14:46 ; Search time 161 Seconds
(without alignments)
762.496 Million cell updates/sec

Title: US-10-650-123-2
Perfect score: 868
Sequence: 1 MKKALATLIALPALAALAE.....VNTKVRSGELSGVRVKF 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	100.0	174	2	P96943 NEIME
2	864	99.5	174	2	Q9P17 NEISSERIA m
3	864	99.5	174	2	Q7DDM2 NEIMB
4	857	98.7	174	2	Q92R1 NEIME
5	854	98.4	174	2	P95372 NEIME
6	854	98.4	174	2	Q7AR60 NEIMA
7	852	98.2	174	2	Q9P18 NEIME
8	846	97.5	174	2	Q9P18 NEIME
9	825	95.0	174	2	P95343 NEIGO
10	824.5	95.0	175	2	P95371 NEIME
11	809.5	93.3	175	2	Q9PA01 NEIGI
12	303.5	35.0	177	2	Q65RV6 MANSM
13	256	29.5	226	2	Q65TE2 MANSM
14	247	28.5	256	2	Q51124 NEIME
15	246.5	28.4	186	2	Q9CM19 PASMU
16	244	28.1	234	2	Q9P19 NEIME
17	244	28.1	234	2	Q07280 NEIME
18	243	28.0	234	2	Q9R18 NEIME
19	242	27.9	260	1	Q9AJ NEIGO
20	241.5	27.8	232	2	Q9K4T9 NEILA
21	241.5	27.8	241	2	Q9AE80 NEIME
22	240.5	27.7	230	2	Q9R9A7 NEIME
23	240.5	27.7	237	1	Q9AK NEIGO
24	240	27.6	241	2	Q9K4T4 NEILA
25	240	27.6	256	2	Q51126 NEIME
26	240	27.6	259	2	Q51125 NEIME
27	239.5	27.6	232	2	Q9R3P5 NEIME
28	239	27.5	260	1	Q9R1 NEIMC
29	238.5	27.5	257	2	Q50929 NEIFV
30	238	27.4	234	2	Q07287 NEIME
31	238	27.4	237	2	O31176 NEIME

32	237	27.3	239	2	Q7BW15 NEIME
33	237	27.3	262	2	O33388 NEIME
34	236.5	27.2	232	2	Q9K4T3 NEISU
35	236.5	27.2	270	1	Q9ROV4 NEIGO
36	236	27.2	270	2	Q9ROV4 NEIME
37	236	27.2	283	2	O50943 NEIGO
38	235	27.1	236	1	Q9AC NEIGO
39	234.5	27.0	241	2	O07274 NEIME
40	234	27.0	240	2	O07925 NEIME
41	234	27.0	272	2	Q51013 NEIGO
42	233.5	26.9	241	2	O07912 NEIME
43	233.5	26.9	253	2	O51303 NEISI
44	233	26.8	233	2	Q9K4T5 NEILA
45	233	26.8	235	2	O30753 NEISSERIA m

ALIGNMENTS

RESULT 1
P96943 NEIME PRELIMINARY; PRT; 174 AA.
AC P96943;
DT 01-MAY-1997 (TREMELrel. 03, Created)
DT 01-MAY-1997 (TREMELrel. 03, Last sequence update)
DT 10-MAY-2005 (TREMELrel. 30, Last annotation update)
DE Outer membrane protein precursor (Surface protein A).
GN Name=nsaA;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=608B;
RX MEDLINE=97253610; PubMed=9104804; DOI=10.1084/jem.185.7.1173;
RA Martin D., Cadieux N., Hamel J., Brodeur B.R.;
RT "Highly conserved Neisseria meningitidis surface protein confers protection against experimental infection.";
RL J. Exp. Med. 185:1173-1183(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.

STRAIN=608B;
MEDLINE=99270944; PubMed=10338491;
Plante M., Cadieux N., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
"Antigenic and molecular conservation of the gonococcal NspA protein.";
Infect. Immun. 67:2855-2861(1999).
[3]
RP NUCLEOTIDE SEQUENCE.
STRAIN=608B;
MEDLINE=99386904; PubMed=10456958;
Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
"Bactericidal and cross-protective activities of a monoclonal antibody directed against Neisseria meningitidis NspA outer membrane protein.";
Infect. Immun. 67:4955-4959(1999).
[4]
RP NUCLEOTIDE SEQUENCE.
STRAIN=M986, NG5/88, and NGP165;
Moe G.N., Tan S., Granoff D.M.;
"Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains.";
Infect. Immun. 0:0-0(1999).
DR EMBL; U52066; AAC36000.1; -; Genomic DNA.
DR EMBL; AF175680; AADS3283.1; -; Genomic DNA.
DR EMBL; AF175682; AADS3285.1; -; Genomic DNA.
DR EMBL; AF175683; AADS3286.1; -; Genomic DNA.
DR HSSP; Q9RP17; 1P4T.
DR SMR; P96943; 20-174.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.

KW Signal.
 FT SIGNAL 1 19 Potential.
 SQ SEQUENCE 174 AA; 18425 MW; E8B02767DDC6F19 CRC64;

Query Match 100.0%; Score 868; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 8.2e-69;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDTYTRYKYNKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
 DB 61 FAVDTYTRYKYNKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120

QY 121 SQTSGIGLVLTGVSVAVTNPVLDAGYRNYIGKVTNKVRSGLSVGVVRKF 174
 DB 121 SQTSGIGLVLTGVSVAVTNPVLDAGYRNYIGKVTNKVRSGLSVGVVRKF 174

RESULT 3
 Q9RP17_NEIME
 ID Q9RP17_NEIME PRELIMINARY; PRT; 174 AA.
 AC Q9RP17;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Surface protein A.
 GN Name=nsa;
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CU385;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A
 among Neisseria meningitidis Group B strains.";
 RL Infect. Immun. 0:0-0(1999).
 DR EMBL; AF175678; AAD53281.1; -; Genomic_DNA.
 DR PIR; G81174; G81174.
 DR PDB; 1P4T; X-ray; A=20-174.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0015288; F:porin activity; IEA.
 DR InterPro; IPR003394; Porin, opacity.
 DR Pfam; PF02462; Opacity; 1.
 SQ SEQUENCE 174 AA; 18397 MW; E8B02767DDC6E109 CRC64;

Query Match 99.5%; Score 864; DB 2; Length 174;
 Best Local Similarity 99.4%; Pred. No. 1.9e-68;
 Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDTYTRYKYNKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
 DB 61 FAVDTYTRYKYNKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120

QY 121 SQTSGIGLVLTGVSVAVTNPVLDAGYRNYIGKVTNKVRSGLSVGVVRKF 174
 DB 121 SQTSGIGLVLTGVSVAVTNPVLDAGYRNYIGKVTNKVRSGLSVGVVRKF 174

RESULT 3
 Q7DDM2_NEIME
 ID Q7DDM2_NEIME PRELIMINARY; PRT; 174 AA.
 AC Q7DDM2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Outer membrane protein NspA.
 GN Name=nsa; OrderedLocuNames=NMB0663;
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=491;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MC58 / Serogroup B;
 RX MEDLINE=20175755; Pubmed=10710307; DOI=10.1126/science.287.5459.1809;
 RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
 RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
 RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
 RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
 RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
 RA Clifton H., Clark E.B., Cotton M.D., Uterback T.R., Khouri H.M.,
 RA Qin H., Vamathevan J.J., Gill J., Scariato V., Masignani V., Pizzo M.,
 RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
 RA Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 MC58";
 RL Science 287:1809-1815(2000).
 DR EMBL; AE002098; AAF410R1.1; -; Genomic_DNA.
 DR SMR; Q7DDM2; 20-174.
 DR TIGR; NMB0663; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0015288; F:porin activity; IEA.
 DR InterPro; IPR003394; Porin, opacity.
 DR Pfam; PF02462; Opacity; 1.
 DR Complete proteome.
 SQ SEQUENCE 174 AA; 18397 MW; E8B02767DDC6E109 CRC64;

Query Match 99.5%; Score 864; DB 2; Length 174;
 Best Local Similarity 99.4%; Pred. No. 1.9e-68;
 Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDTYTRYKYNKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
 DB 61 FAVDTYTRYKYNKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120

QY 121 SQTSGIGLVLTGVSVAVTNPVLDAGYRNYIGKVTNKVRSGLSVGVVRKF 174
 DB 121 SQTSGIGLVLTGVSVAVTNPVLDAGYRNYIGKVTNKVRSGLSVGVVRKF 174

RESULT 4
 Q9R2R1_NEIME
 ID Q9R2R1_NEIME PRELIMINARY; PRT; 174 AA.
 AC Q9R2R1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Surface protein A.
 GN Name=nsa;
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=M136, and B232;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A
 among Neisseria meningitidis Group B strains.";
 RL Infect. Immun. 0:0-0(1999).
 DR EMBL; AF175679; AAD53282.1; -; Genomic_DNA.
 DR EMBL; AF175677; AAD53280.1; -; Genomic_DNA.
 DR HSP; Q9RP17; 1P4T.

DR SMR; Q9R2R1; 20-174.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR003394; Porin activity; IEA.
 DR Pfam; PF02462; Opacity; 1.
 SQ SEQUENCE 174 AA; 18395 MW; ECF6F39A9286910E CRC64;
 Query Match 98.7%; Score 857; DB 2; Length 174;
 Best Local Similarity 98.3%; Pred. No. 7.8e-68;
 Matches 171; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 Qy 61 FAVDYTRYKNYKAPSTDFPKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120
 Db 61 FAVDYTRYKNYKAPSTDFPKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120
 Qy 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKVTNKVRSGLSVGVVRVKF 174
 Db 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKVTNKVRSGLSVGVVRVKF 174

RESULT 5
 P95372 NEIME
 ID P95372 NEIME PRELIMINARY; PRT; 174 AA.
 AC P95372;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Outer membrane protein precursor.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=Z4063;
 RX MEDLINE=9386904; PubMed=10456958;
 RA Cadioux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
 RT "Bactericidal and cross-protective activities of a monoclonal antibody
 RL directed against Neisseria meningitidis Napa outer membrane protein.";
 DR EMBL; U52068; AAB41580.1; -; Genomic_DNA.
 DR PIR; B81932; B81932.
 DR HSP; Q9RP17; 1P4F.
 DR SMR; P95372; 20-174.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR003394; Porin activity; IEA.
 DR Pfam; PF02462; Opacity; 1.
 KW Signal.
 FT SIGNAL
 SQ SEQUENCE 174 AA; 18355 MW; E8A4A1ADA4F6F009 CRC64;

Query Match 98.4%; Score 854; DB 2; Length 174;
 Best Local Similarity 98.3%; Pred. No. 1.4e-67;
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 Qy 61 FAVDYTRYKNYKAPSTDFPKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120
 Db 61 FAVDYTRYKNYKAPSTDFPKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120
 Qy 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKVTNKVRSGLSVGVVRVKF 174
 Db 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKVTNKVRSGLSVGVVRVKF 174

RESULT 6
 Q7AR60 NEIMA
 ID Q7AR60 NEIMA PRELIMINARY; PRT; 174 AA.
 AC Q7AR60;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)
 DE Outer membrane protein.
 GN Name=napA; OrderedLocuNames=NMA0862;
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=63699;
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
 RX MEDLINE=2022556; PubMed=10761919; DOI=10.1038/35006655;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrell B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 RL meningitidis Z2491."
 DR EMBL; AL462754; CAB84143.1; -; Genomic_DNA.
 DR SMR; Q7AR60; 20-174.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0015288; F:porin activity; IEA.
 DR InterPro; IPR003394; Porin opacit.
 DR Pfam; PF02462; Opacity; 1.
 KW Complete proteome.
 SQ SEQUENCE 174 AA; 18355 MW; E8A4A1ADA4F6F009 CRC64;

Query Match 98.4%; Score 854; DB 2; Length 174;
 Best Local Similarity 98.3%; Pred. No. 1.4e-67;
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 Qy 61 FAVDYTRYKNYKAPSTDFPKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120
 Db 61 FAVDYTRYKNYKAPSTDFPKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120
 Qy 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKVTNKVRSGLSVGVVRVKF 174
 Db 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKVTNKVRSGLSVGVVRVKF 174

RESULT 7
 Q9RP16 NEIME
 ID Q9RP16 NEIME PRELIMINARY; PRT; 174 AA.
 AC Q9RP16;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Surface protein A.
 GN Name=napA;
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=NG3/88;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A
 RL among Neisseria meningitidis Group B strains.";
 DR Infect. Immun. 0:0-0(1999).
 DR EMBL; AF175681; AAD53284.1; -; Genomic_DNA.

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DR HSSP; Q9RP17; 1P4T.
DR SMR; Q9RP16; 20-174.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
SQ SEQUENCE 174 AA; 18355 MW; ECF6F38B9286800E CRC64;

Query Match 98.2%; Score 852; DB 2; Length 174;
Best Local Similarity 97.7%; Pred. No. 2.2e-67;
Matches 170; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
Qy 121 SQTSGIGLVLTGVSAYVTPNVLDAGYRNYIGKVTNKVRSGLSAGYRVRVKF 174
Db 121 SQTSGIGLVLTGVSAYVTPNVLDAGYRNYIGKVTNKVRSGLSAGYRVRVKF 174

RESULT 8
Q9RP18_NEIME
ID Q9RP18_NEIME PRELIMINARY; PRT; 174 AA.
AC Q9RP18;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Surface protein A.
GN Name=nspp;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=8047;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0(1999).
DR EMBL; AF175676; AA053279.1; -; Genomic_DNA.
DR HSSP; Q9RP17; 1P4T.
DR SMR; Q9RP18; 20-174.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
SQ SEQUENCE 174 AA; 18357 MW; 0205AA1DA1B7F005 CRC64;

Query Match 97.5%; Score 846; DB 2; Length 174;
Best Local Similarity 97.1%; Pred. No. 7.3e-67;
Matches 169; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
Qy 121 SQTSGIGLVLTGVSAYVTPNVLDAGYRNYIGKVTNKVRSGLSAGYRVRVKF 174
Db 121 SQTSGIGLVLTGVSAYVTPNVLDAGYRNYIGKVTNKVRSGLSAGYRVRVKF 174

RESULT 9
P95343_NEIGO
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ID P95343_NEIGO PRELIMINARY; PRT; 174 AA.
AC P95343;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Outer membrane protein precursor (Surface protein A).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B2;
RX MEDLINE=9270944; PubMed=10338491;
RA Plante M., Cadieux N., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
RT "Antigenic and molecular conservation of the gonococcal NspA
protein.";
RL Infect. Immun. 67:2855-2861(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WHO-A;
RA Mingchun J.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U52069; AAB41581.1; -; Genomic_DNA.
DR EMBL; AY157539; AAN77898.1; -; Genomic_DNA.
DR HSSP; Q9RP17; 1P4T.
DR SMR; P95343; 20-174.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
KW Signal.
FT SIGNAL 1 19 Potential.
SQ SEQUENCE 174 AA; 18337 MW; 1B558EC8A040841A CRC64;

Query Match 95.0%; Score 825; DB 2; Length 174;
Best Local Similarity 94.3%; Pred. No. 5.3e-65;
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
Qy 121 SQTSGIGLVLTGVSAYVTPNVLDAGYRNYIGKVTNKVRSGLSAGYRVRVKF 174
Db 121 SQTSGIGLVLTGVSAYVTPNVLDAGYRNYIGKVTNKVRSGLSAGYRVRVKF 174

RESULT 10
P95371_NEIME
ID P95371_NEIME PRELIMINARY; PRT; 175 AA.
AC P95371;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Outer membrane protein precursor.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MCH 88;
RX MEDLINE=99386904; PubMed=10456958;
RA Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
RT "Bactericidal and cross-protective activities of a monoclonal antibody
directed against Neisseria meningitidis NspA outer membrane protein.";
RL Infect. Immun. 67:4955-4959(1999).
DR EMBL; U52067; AAB41579.1; -; Genomic_DNA.
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DR HSP; Q9RPI7; 1P4T.
DR SMR; P95371; 20-175.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 175 AA; 18572 MW; D1EA8P2FP5CC2FEA CRC64;

Query Match 95.0%; Score 824.5; DB 2; Length 175;
Best Local Similarity 95.4%; Pred. No. 5.9e-65;
Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALALIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYK-APSTDPFKLYSGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDS 119
Db 61 FAVDYTRYKNYKQVPSTDPFKLYSGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDS 120

Qy 120 FSQTSIGLGLVLTGVSAYTPNVLDAGYRNYIGKNTVKNVRSGLSVGVKVF 174
Db 121 FSQTSIGLGLVLTGVSAYTPNVLDAGYRNYIGKNTVKNVRSGLSVGVKVF 175

RESULT 11
Q5FA01_NEIG1 PRELIMINARY; PRT; 175 AA.
AC Q5FA01;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Outer membrane protein.
GN OrderedLocusNames=NG002333;
OS Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=242231;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Lewis L.A., Gillaspay A.P., McLaughlin R.E., Gipson M., Ducey T.F.,
RA Ownbey T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,
RA Song L., Lin S., Yuan X., Najjar F., Zhan M., Ren Q., Zhu H., Qi S.,
RA Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;
RT "The complete genome sequence of Neisseria gonorrhoeae."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB004969; AAN88986.1; -; Genomic_DNA.
DR InterPro; IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
KW Complete proteome.
SQ SEQUENCE 175 AA; 18478 MW; 44C05922D87FACF8 CRC64;

Query Match 93.3%; Score 809.5; DB 2; Length 175;
Best Local Similarity 93.1%; Pred. No. 1.3e-63;
Matches 163; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALALIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYK-APSTDPFKLYSGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDS 119
Db 61 FAVDYTRYKNYKQVPSTDPFKLYSGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDS 120

Qy 120 FSQTSIGLGLVLTGVSAYTPNVLDAGYRNYIGKNTVKNVRSGLSVGVKVF 174
Db 121 FSKTSAGLGLVLTGVSAYTPNVLDAGYRNYIGKNTVKNVRSGLSVGVKVF 175

RESULT 12
Q65RV6_MANS PRELIMINARY; PRT; 177 AA.
AC Q65RV6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=MS1697;
OS Mannheimia succiniciproducens (strain MBEL55E).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15378067; DOI=10.1038/nbt1010;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
succiniciproducens."
RL Nat. Biotechnol. 22:1275-1281(2004).
DR EMBL; AB016827; AAU37768.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.

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ID Q65RV6_MANS PRELIMINARY; PRT; 177 AA.
AC Q65RV6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=MS1697;
OS Mannheimia succiniciproducens (strain MBEL55E).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15378067; DOI=10.1038/nbt1010;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
succiniciproducens."
RL Nat. Biotechnol. 22:1275-1281(2004).
DR EMBL; AB016827; AAU37768.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.

Query Match 35.0%; Score 303.5; DB 2; Length 177;
Best Local Similarity 40.2%; Pred. No. 8.1e-19;
Matches 74; Conservative 25; Mismatches 88; Indels 17; Gaps 6;

Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 59
Db 1 MKKTLALIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 56

Qy 60 FPAVDYTRYKNYKAPSTDPFKLYSGASAIYDFDTQSPVKPYLGARLSLNRSASVDL 114
Db 57 RYADYTHYKSTGDNSEVKAHGFVSAIYDIEVGSVPKPYIGARLSAN--DIDAKBEKR 114

Qy 115 -GGSDSFSQT---SIGLGLVLTGVSAYTPNVLDAGYRNYIGKNTVKNVRSGLSVGV 170
Db 115 SGGSRIRKETSDSKYLGALAGVQYQAKDVSGLNGVVEYNELKANG-HNINQYKARVGV 173

Qy 171 RVKF 174
Db 174 RYDF 177

RESULT 13
Q65TE2_MANS PRELIMINARY; PRT; 226 AA.
AC Q65TE2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=MS1161;
OS Mannheimia succiniciproducens (strain MBEL55E).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15378067; DOI=10.1038/nbt1010;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
succiniciproducens."
RL Nat. Biotechnol. 22:1275-1281(2004).
DR EMBL; AB016827; AAU37768.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.

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DR Pfam; PF02462; Opacity; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 226 AA; 25460 MW; 106C558F9B4C1504 CRC64;

Query Match 29.5%; Score 256; DB 2; Length 226;
 Best Local Similarity 35.1%; Pred. No. 1.7e-14;
 Matches 72; Conservative 26; Mismatches 67; Indels 40; Gaps 8;

QY 1 MKKALATLIALPAAALAEAGS-GFYVQADAAHAKASSLSGSAKG-----FSPR 49
 DB 31 MKK---TTLAIVAIGALIAISSASANWYVQGDVGYSKIKAS-----GMDLLDPKDNVFDQR 82
 QY 50 ISAGYRINDLPAVDYTRYKNYK-----APSTDFKLYSIGASAIYDFDTQSP 96
 DB 83 ISAGYDFGDIRLAVDYSHIGRAKADHYTLFRGEQWETSGSTSVETNSFGISAIYDFNLNTS 142
 QY 97 VKPYLGARLSLRASV-----DLGSDSPSQ--TSIGLGVLTVGSYAVTPNVLDAGYRY 149
 DB 143 LMPYVGVRLSNSLKFEDHWRDNGASESYSETKTKFGYGALAGVQYHLTDNLLNNGVEY 202
 QY 150 NYIGKAVNTVKNVRSGLSVGVKPF 174
 DB 203 NRLGKVEVK-IHOYSAKAGLRYNP 226

RESULT 14
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 AC Q51124;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Opacity outer membrane protein (Fragment).
 GN Name: opa;
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Z4197;
 RX MEDLINE=98129089; PubMed=9467908;
 RA Hobbs M.M., Malorny B., Prasad P., Morelli G., Kusecek B.,
 RA Heckels J.E., Cannon J.G., Achtman M.;
 RT "Recombinational reassortment among opa genes from ET-37 complex
 RT Neisseria meningitidis isolates of diverse geographical origins.";
 RL Microbiology 144:157-166(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC PubMed=3123389;
 RA Kawula T.H., Aho E.L., Barritt D.S., Klapper D.G., Cannon J.G.;
 RT "Reversible phase variation of expression of Neisseria meningitidis
 RT class 5 outer membrane proteins and their relationship to gonococcal
 RT proteins II.";
 RL Infect. Immun. 56:380-386(1988).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=92157869; PubMed=1787795;
 RA Aho E.L., Dempsey J.A., Hobbs M.M., Klapper D.G., Cannon J.G.;
 RT "Characterization of the opa (class 5) gene family of Neisseria
 RT meningitidis.";
 RL Mol. Microbiol. 5:1429-1437(1991).
 DR EMBL; U37255; AAC46101.1; -; Genomic_DNA.
 DR PIR; B60119; B60119.
 DR PIR; S77737; S77737.
 DR HSSP; Q9RP17; 1P4T.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0015288; F:porin activity; IEA.
 DR InterPro; IPR003394; Porin_opacity.
 DR Pfam; PF02462; Opacity; 1.
 FT NON_TER
 SQ SEQUENCE 256 AA; 28335 MW; 9D41C6079C6DD13P CRC64;

Query Match 28.5%; Score 247; DB 2; Length 256;
 Best Local Similarity 28.3%; Pred. No. 1.3e-13;
 Matches 69; Conservative 33; Mismatches 64; Indels 78; Gaps 7;

QY 8 LIALALPAAALAEAGSGFYVQADAAHA-----KASSLSG-----AKGFS 47
 DB 14 LPSAAQAASESDGHGPFYVQADLAYAAERITHDPKATGANNNTSTVSDYFRNIRAHSH 73
 QY 48 PRISAGYRINDLPAVDYTRYK-----NYKAPSTDFK-----LYS 82
 DB 74 PRVSVGVDFCGWRIADYASYRWKBSNSSTKKVTEADIADNYKETKTEHQNGSFFHAAS 133
 QY 83 IGASAIYDFDTQSPVXPYLGARLSLR-----ASVDLGG----- 116
 DB 134 LGLSAIYDFKLNDFKFPYIGARVAYGHVQHVHVSVEKTTTNTVTSKPTATSPQGGPIITQD 193
 QY 117 -----SDSPQTSIGLGVLTVGSYAVTPNVLDAGYRYNYIGKAVNTVKNVRSGLSVG 170
 DB 194 PSKPPYHSHSISLSGLGVIAGVGFDITPKTLTDTGYRYHNWGRLENT-RFKTHEVSLGM 252
 QY 171 RVKPF 174
 DB 253 RYRP 256

RESULT 15
 Q9CM19_PASMU PRELIMINARY; PRT; 186 AA.
 AC Q9CM19;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Opa.
 GN Name: opa; OrderedLocusNames=PM1025;
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Pm70;
 RX MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida Pm70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 DR EMBL; AE006143; AAK03109.1; -; Genomic_DNA.
 DR HSSP; Q9RP17; 1P4T.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0015288; F:porin activity; IEA.
 DR InterPro; IPR003394; Porin_opacity.
 DR Pfam; PF02462; Opacity; 1.
 KW Complete proteome.
 SQ SEQUENCE 186 AA; 20512 MW; 1B17F0A4ACFC0157 CRC64;

Query Match 28.4%; Score 246.5; DB 2; Length 186;
 Best Local Similarity 32.3%; Pred. No. 9.6e-14;
 Matches 61; Conservative 32; Mismatches 77; Indels 19; Gaps 5;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAK-----ASSLSGSAKSPRISAGYRIN 57
 DB 2 MKK---SLVLAITGALCSLTASANFYVQGDVGAKTKFSSYSEMNKTNIYPNVSVGYDLG 58
 QY 58 DLRFPAVDYTRYKNYKAPS-----TDFKLYSIGASAIYDFDTQSPVXPYLGARLSLN 108
 DB 59 AMRLALDYTHYGFSGTSIFGVNQKEHVSTKIYGLGLSAFYDFNINSVLFPYVGMRLASN 118
 QY 109 RASVDLGGSDSP---SQTSLGLVLTVGSYAVTPNVLDAGYRYNYIGKAVNTVKNVRSGE 165
 DB 119 IPDIENKGSNFRSEKTKTKLGYGFIAGAOYGLMTNLFVNGGIEYRNLGRFSDT-SVNQYG 177
 QY 166 LSVGVKVP 174
 DB 178 AKVGLRYDF 186

Search completed: January 11, 2006, 15:21:28
Job time : 163 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 11, 2006, 15:16:52 ; Search time 45 Seconds
(without alignments)
319.679 Million cell updates/sec

Title: US-10-650-123-2

Perfect score: 868

Sequence: 1 MKKALATLIALPALAALAE.....VNTVKNVRSGELSGVGRVKF 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA.*
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2: /cgn2_6/ptodata/1/1aa/6-COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/H-COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/PCUTUS-COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	868	100.0	174	2	US-08-913-362-2
2	854	98.4	174	2	US-08-913-362-6
3	838.5	96.6	175	2	US-08-913-362-30
4	825	95.0	174	2	US-08-913-362-8
5	824.5	95.0	175	2	US-08-913-362-4
6	135	15.6	170	1	US-08-127-499A-20
7	135	15.6	170	1	US-08-482-847-20
8	133	15.3	25	2	US-08-913-362-26
9	113.5	13.1	98	2	US-09-540-236-2245
10	109.5	12.6	187	2	US-09-489-039A-13659
11	104.5	12.0	384	2	US-09-543-681A-7922
12	93	10.7	190	2	US-09-543-681A-7684
13	92.5	10.7	261	2	US-09-252-991A-19759
14	89.5	10.3	186	2	US-09-540-236-2792
15	89.5	10.3	385	2	US-09-489-039A-7451
16	88.5	10.2	180	2	US-09-164-714-7
17	88.5	10.2	573	2	US-09-336-447A-3
18	88.5	10.2	573	2	US-09-952-267B-3
19	88	10.1	359	1	US-08-457-997B-2
20	88	10.1	359	2	US-08-467-722A-2
21	88	10.1	359	2	US-09-451-184-2
22	88	10.1	397	2	US-09-902-540-16267
23	88	10.1	610	2	US-09-336-447A-11
24	88	10.1	610	2	US-09-952-267B-11
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27	88	10.1	889	2	US-09-336-447A-15

28	88	10.1	889	2	US-09-952-267B-15
29	87.5	10.1	708	2	US-09-336-115C-2
30	87	10.0	16	2	US-08-913-362-15
31	87	10.0	500	2	US-09-325-932A-149
32	86	9.9	512	2	US-09-059-584-57
33	85.5	9.9	238	2	US-09-902-540-12284
34	85.5	9.9	487	2	US-09-328-352-5331
35	85	9.8	568	4	PCT-US95-13749-5
36	84.5	9.7	643	2	US-09-328-352-5146
37	84	9.7	351	2	US-09-252-991A-30094
38	83.5	9.6	721	2	US-09-328-352-7781
39	83	9.6	364	2	US-09-418-980-8
40	83	9.6	364	2	US-09-809-665A-151
41	83	9.6	364	2	US-09-506-078-45
42	82	9.4	172	2	US-09-902-540-14682
43	82	9.4	433	1	US-08-883-515-2
44	82	9.4	433	2	US-09-770-509-27
45	82	9.4	512	2	US-09-059-584-56

ALIGNMENTS

RESULT 1
US-08-913-362-2
; Sequence 2, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Joseph
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-913-362-2

Query Match 100.0% Score 868; DB 2; Length 174;

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Best Local Similarity 100.0%; Pred. No. 5.9e-93;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRRASVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRRASVDLGGSDSF 120

Qy 121 SQTSGIGLVLTGVSAYVTPNVLDAGRYNYIGKVNTVKNVRSGLSVGVRVKF 174
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Db 121 SQTSGIGLVLTGVSAYVTPNVLDAGRYNYIGKVNTVKNVRSGLSVGVRVKF 174

RESULT 2
US-08-913-362-6
; Sequence 6, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913.362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406.362
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER: US 60/001.983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-913-362-6

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Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRRASVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRRASVDLGGSDSF 120

Qy 121 SQTSGIGLVLTGVSAYVTPNVLDAGRYNYIGKVNTVKNVRSGLSVGVRVKF 174
Db 121 SQTSGIGLVLTGVSAYVTPNVLDAGRYNYIGKVNTVKNVRSGLSVGVRVKF 174

Qy 121 SQTSGIGLVLTGVSAYVTPNVLDAGRYNYIGKVNTVKNVRSGLSVGVRVKF 174
Db 121 SQTSGIGLVLTGVSAYVTPNVLDAGRYNYIGKVNTVKNVRSGLSVGVRVKF 174

RESULT 3
US-08-913-362-30
; Sequence 30, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913.362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406.362
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER: US 60/001.983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-913-362-30

Query Match 96.6%; Score 838.5; DB 2; Length 175;
Best Local Similarity 97.1%; Pred. No. 1.6e-89;
Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRRASVDLGGSDS 119
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRRASVDLGGSDS 120

Qy 120 PSQTSIGLVLTGVSAYVTPNVLDAGRYNYIGKVNTVKNVRSGLSVGVRVKF 174
Db 120 PSQTSIGLVLTGVSAYVTPNVLDAGRYNYIGKVNTVKNVRSGLSVGVRVKF 174
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Db 121 FSQTSXGLGLVAGSVYAVTPNVDLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 175

RESULT 4

US-08-913-362-8

; Sequence 8, Application US/08913362

; Patent No. 6287574

; GENERAL INFORMATION:

; APPLICANT: Brodeur, Bernard R

; APPLICANT: Martin, Denis

; APPLICANT: Hamel, Josee

; APPLICANT: Rioux, Clement

; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN

; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/913,362

; FILING DATE: 13-NOV-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/406,362

; FILING DATE: 17-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/001,983

; FILING DATE: 04-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Bent, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 047998/0128

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 174 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-913-362-8

Query Match 95.0%; Score 825; DB 2; Length 174;

Best Local Similarity 94.3%; Pred. No. 6.1e-88;

Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVLDGSDSF 120

Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVLDGSDSF 120

Qy 121 SQTSLGLVLTGVSAYVTPNVDLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 174

Db 121 SKTSAGLGLVAGSVYAVTPNVDLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 174

RESULT 5

US-08-913-362-4

; Sequence 4, Application US/08913362

; Patent No. 6287574

; GENERAL INFORMATION:

; APPLICANT: Brodeur, Bernard R

; APPLICANT: Martin, Denis

; APPLICANT: Hamel, Josee

; APPLICANT: Rioux, Clement

; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN

; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/913,362

; FILING DATE: 13-NOV-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/406,362

; FILING DATE: 17-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/001,983

; FILING DATE: 04-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Bent, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 047998/0128

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 175 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-913-362-4

Query Match 95.0%; Score 824.5; DB 2; Length 175;

Best Local Similarity 95.4%; Pred. No. 7e-88;

Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVLDGSDS 119

Db 61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDFNGSDS 120

Qy 120 FSQTSIGLVLTVGSYAVTPNVDLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 174

Db 121 FSQSTGLVGLVAGSVYAVTPNVDLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 175

RESULT 6

US-08-127-499A-20

; Sequence 20, Application US/08127499A

; Patent No. 5510264

; GENERAL INFORMATION:

; APPLICANT: VAN ALSTYNE, Diane

; APPLICANT: SHARMA, Lawrence Rajendra

; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED

; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

```

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-482-847-20

Query Match 15.6%; Score 135; DB 1; Length 170;
Best Local Similarity 26.3%; Pred. NO. 1.4e-07;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATTLALALPAALAGASGFFYQDAAH-----AKASSSLGS-----AKG 45
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 15 SLLSFSSAAQASEDRRSPYYQADLAYAAERITHDYPOATGANNTSTVSDYFRNIRAH 74
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 46 FSPRISAGVRINDLRFADVDTYKYN-----KAPSTDFK 79
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 75 IHPRVSVGVDFGWRIAADYASRYKNNNKYSVNTKELNKKKKDLKTENQENGTFHA 134
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 80 LYSIGASAIYDPTQSPVKPYLGARLSLN--RASVD 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 135 ASSLGLSALIYDFKLKGFKPYIGARVAYGVHVSID 170

RESULT 8
US-08-913-362-26
; Sequence 26, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768

```

REFERENCE/DOCKET NUMBER: 047998/0128
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: Neisseria meningitidis
STRAIN: 608B
US-08-913-362-26

Query Match 15.3%; Score 133; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGA 85
Db 1 FAVDYTRYKNYKAPSTDFKLYSIGA 25

RESULT 9
US-09-540-236-2245
Sequence 2245, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2245
LENGTH: 98
TYPE: PRT
ORGANISM: M.catarrhalis
US-09-540-236-2245

Query Match 13.1%; Score 113.5; DB 2; Length 98;
Best Local Similarity 37.9%; Pred. No. 1.9e-05;
Matches 22; Conservative 13; Mismatches 18; Indels 5; Gaps 2;

Qy 122 QTSIGLVLTGVSVAVTNVDLAGYRNYIG---KNTVKNVRSGE--LSGVVRVKF 174
Db 41 ETKVGFVLAGAQAQVAINPQLSDAGVEYNILGKYDKLDTASKLKAHOYCAKVGRLRHF 98

RESULT 10
US-09-489-039A-13699
Sequence 13699, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13699
LENGTH: 187
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13699

Query Match 12.6%; Score 109.5; DB 2; Length 187;

Best Local Similarity 25.2%; Pred. No. 0.00015;
Matches 51; Conservative 26; Mismatches 78; Indels 47; Gaps 7;
Qy 1 MKKALATLIA--LALPAAALAEAGSGFYVQADAAHAKASSIGSAK-----44
Db 5 MKSIAAKWVAVTIALGASSAACAAVNLHGEAGFTNLSAFGAGEPGMTFSSQWAHSDN 64
Qy 45 -GFSPRISAGYRINDLRFVADYTRYKNYKAPSTDFKLYSIGASAIY-----DFDTQSPVKP 99
Db 65 DGDSVGLGMGYNFGNLPF-----LMTLGGKAVYLNPKDGDGYATAA 106
Qy 100 YLGARLSINRASVDLGGSDSPQSISIGLV-----LTGVSVAVTNVDLDAGYRY-NYI 152
Db 107 GGGAELPLGQ-YFTLFGEGYSPDSMSSGVEDYVEANAGVRLNVRPSLNIEAGYRIIDMA 165
Qy 153 GKAVTVKNVRSGELSGVVRVKF 174
Db 166 GKDGNEDNTLADGAYAGVNF 187

RESULT 11
US-09-543-681A-7922
Sequence 7922, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7922
LENGTH: 384
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-7922

Query Match 12.0%; Score 104.5; DB 2; Length 384;
Best Local Similarity 26.1%; Pred. No. 0.0017;
Matches 55; Conservative 27; Mismatches 86; Indels 43; Gaps 13;

Qy 1 MKKALATLIAALPAAALAEAGSG-----FYQADAAHAKASS-----SLGSAKGF 46
Db 23 MKK---TALALAVAAFAATAQAAPKONTWYTGKLGWSQYQSTGNNWDGWNIGSGTH 79
Qy 47 SPRIS----AGYRIND---LRFVADYTRYKNYKAPSTD--FKLYSIGASAIYDFDTQSPV 97
Db 80 KDQIGAGAFAGYQYNQVGLFELGYDNLGRMAYKGSYNNGAFAKQGIQLTTKLSPVMDL 139
Qy 98 KPY--LGARL-----SLNRASVDLGGSDSPQSISIGLVL--TGVSVAVTNVDLDAG 146
Db 140 DVTYTLGGWVRADSTATINATSA--GTQKFSENDTGVSPVFAITGTATPNTATRL 197
Qy 147 YRY-NYIGKVTNVR--SGELSGVVRVKF 174
Db 198 YQWNNIGDKCTL-NARPDNGLSVGVAYRF 227

RESULT 12
US-09-543-681A-7684
Sequence 7684, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706

Qy 129 VLTGVSYAVTPNVLDAGRY-NYIGKVTY-KNVRSGELSVGRVKF 174
Db 183 FAGGVWAVTRDIATRLRYQWVNNIGDAGTVGTRPDNGMLSLGVSYRF 230

Search completed: January 11, 2006, 15:23:15
Job time : 46 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2006, 19:49:08 ; Search time 3313 Seconds
(without alignments)
9007.791 Million cell updates/sec

Title: US-10-650-123-1

Perfect score: 525

Sequence: 1 atgaaaaagcactgtccac.....gcgtgcgcgtcaaatctga 525

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5893141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_atc.*

11: gb_sy.*

12: gb_un.*

13: gb_vl.*

14: gb_hgt.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	525	100.0	525	1 AF175682	AF175682 Neisseria
3	525	100.0	525	1 AF175683	AF175683 Neisseria
4	525	100.0	525	6 CQ786532	CQ786532 Sequence
5	525	100.0	525	6 CQ814512	CQ814512 Sequence
6	525	100.0	830	1 NMU52066	U52066 Neisseria m
7	525	100.0	830	6 AF167414	AF167414 Sequence
8	521.8	99.4	525	1 AF175678	AF175678 Neisseria
9	521.8	98.4	110000	1 AE002098_06	Continuation (7 of
10	521.8	99.4	349980	6 AX044030	AX044030 Sequence
11	518.6	98.8	850	1 NMU52068	U52068 Neisseria m
12	518.6	98.8	850	6 AF167416	AF167416 Sequence
13	518.6	98.8	311321	1 NMA322491	AF162754 Neisseria
14	517	98.5	525	1 AF175677	AF175677 Neisseria
15	517	98.5	525	1 AF175679	AF175679 Neisseria
16	515.4	98.2	525	1 AF175676	AF175676 Neisseria
17	515.4	98.2	525	1 AF175681	AF175681 Neisseria
18	502.6	95.7	525	1 AY157539	AY157539 Neisseria

19	502.6	95.7	710	1 NGU52069	U52069 Neisseria g
20	502.6	95.7	710	6 AX685933	AX685933 Sequence
21	502.6	95.7	810	6 AR167417	AR167417 Sequence
22	501.2	95.5	528	6 AR167420	AR167420 Sequence
23	491.2	93.6	710	1 NMU52067	U52067 Neisseria m
24	491.2	93.6	710	6 AR167415	AR167415 Sequence
25	483.2	92.0	110000	1 AE004969_02	Continuation (3 of
26	464.8	88.5	468	6 CQ814510	CQ814510 Sequence
27	63	12.0	75	6 CQ771466	CQ771466 Sequence
28	60	11.4	110000	1 BX571966_01	Continuation (2 of
29	59.6	11.4	344615	1 BX569695	BX569695 Synchoco
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32	53.6	10.2	1489	15 AK106151	AK106151 Oryza sat
33	53.6	10.2	1622	15 AK067529	AK067529 Oryza sat
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35	53.6	10.2	159509	15 AP004225	AP004225 Oryza sat
36	53.6	10.2	172642	15 AP004258	AP004258 Oryza sat
37	52.4	10.0	110000	14 AP006490_0	AP006490 Cyanidios
38	51	9.7	110000	1 BA000030_00	BA000030 Streptomy
39	50.2	9.6	749	13 NPO8PT2	NPO8PT2
40	50.2	9.6	969	1 PFR535197	AF535197 Propionib
41	50.2	9.6	1973	15 AK109523	AK109523 Oryza sat
42	50.2	9.6	3196	15 AB077993	AB077993 Oryza sat
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ALIGNMENTS

AF175680 AF175680 525 bp DNA linear BCT 06-SEP-1999
Neisseria meningitidis strain M986 surface protein A (nspA) gene,
complete cds.

AF175680 AF175680
AF175680.1 GI:5825535

Neisseria meningitidis

Neisseria meningitidis

Bacteria; Proteobacteria; Betaproteobacteria; Neisseria

Neisseriaceae; Neisseria.

(bases 1 to 525)

Moe, G.R., Tan, S. and Granoff, D.M.

Differences in Surface Expression of Neisserial Surface Protein A

among Neisseria meningitidis Group B strains

Infect Immun. (1999) in press

2 (bases 1 to 525)

Moe, G.R., Tan, S. and Granoff, D.M.

Direct Submission

Submitted (04-AUG-1999) Children's Hospital Oakland Research

Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA

FEATURES

source

1. 525

/organism="Neisseria meningitidis"

/mol_type="genomic DNA"

/strain="M986"

/db_xref="taxon:487"

1. 525

/gene="nspA"

/gene="nspA"

/codon_start=1

/translation="surface protein A"

/protein_id="AAD53283.1"

/db_xref="GI:5825535"

/translation="MKKALATLIALPAPALAGSGFYVQADAAHAKASSLSGAK

GFSFRSAGYRINDLRFAVDTRYKNYKAPSTDPLKYSIGSALYDFTQSPVKYLG

ARLSLNRAVDLGGDSFSQTSIGLVLTGVSIVATPVNDLDAGRYNYIKGVTKVN

VRSGELSGVGRVKP"

ORIGIN	CDS
Query Match	100.0%; Score 525; DB 1; Length 525;
Best Local Similarity	100.0%; Pred. No. 1.2e-89;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 ATGAAAAAGACATTGCCACACTGATTGCCCTCGCTCTCCGGCGCGCACTGCGGAA 60
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Qy	61 GCGCATCCGGCTTTTACGTCAAGCCGATCGCGCACACGCAAAAGCTCAAGCTCTTTA 120
Db	61 GCGCATCCGGCTTTTACGTCAAGCCGATCGCGCACACGCAAAAGCTCAAGCTCTTTA 120
Qy	121 GGTCTGCAAGGCTTCAGCCCGCATCTCCGAGGCTACCGCATCAACGACCTCGC 180
Db	121 GGTCTGCAAGGCTTCAGCCCGCATCTCCGAGGCTACCGCATCAACGACCTCGC 180
Qy	181 TTCCCGTCGATTACACGCGCTACAAAACCTATAAGCCCATCCACGATTTCAAACTT 240
Db	181 TTCCCGTCGATTACACGCGCTACAAAACCTATAAGCCCATCCACGATTTCAAACTT 240
Qy	241 TACAGCATCGCGGTCGCGCATTTACGATTCGACACCCCAATCGCCGTCACACCGTAT 300
Db	241 TACAGCATCGCGGTCGCGCATTTACGATTCGACACCCCAATCGCCGTCACACCGTAT 300
Qy	301 CTCCGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTGGCGGCGAGCAGCTTC 360
Db	301 CTCCGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTGGCGGCGAGCAGCTTC 360
Qy	361 AGCCAACTCCATCGGCTCGCGTATGACGGCGTAAAGCTATGCGTTACCCCGAAT 420
Db	361 AGCCAACTCCATCGGCTCGCGTATGACGGCGTAAAGCTATGCGTTACCCCGAAT 420
Qy	421 GTCGATTGGATCGCGCTACCGTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480
Db	421 GTCCGTTCCGCGAAGCTGTCGTCGGCTGCGCGTCAAAATCTGA 525
Qy	481 GTCCGTTCCGCGAAGCTGTCGTCGGCTGCGCGTCAAAATCTGA 525
Db	481 GTCCGTTCCGCGAAGCTGTCGTCGGCTGCGCGTCAAAATCTGA 525
RESULT 2	
AF175682	AF175682
LOCUS	Neisseria meningitidis strain NG6/88 surface protein A (nspA) gene, complete cds.
DEFINITION	AF175682.1 GI:5825540
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	Neisseria meningitidis
ORGANISM	Neisseria meningitidis
REFERENCE	Neisseria meningitidis
AUTHORS	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
TITLE	Neisseriaceae; Neisseria.
JOURNAL	Moe, G.R., Tan, S. and Granoff, D.M.
REFERENCE	Differences in Surface Expression of Neisserial Surface Protein A
AUTHORS	Infect. Immun. (1999) In press
JOURNAL	among Neisseria meningitidis Group B strains
TITLE	Direct Submission
AUTHORS	Moe, G.R., Tan, S. and Granoff, D.M.
JOURNAL	Submitted (04-AUG-1999) Children's Hospital Oakland Research
FEATURES	Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
source	Location/Qualifiers
1. .525	/organism="Neisseria meningitidis"
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TITLE Direct Submission
JOURNAL Submitted (04-AUG-1999) Children's Hospital Oakland Research Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
FEATURES Location/Qualifiers
source 1..525
/organism="Neisseria meningitidis"
/mol_type="genomic DNA"
/strain="NGP165"
/db_xref="taxon:487"
gene 1..525
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CDS 1..525
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ORIGIN
Query Match 100.0%; Score 525; DB 1; Length 525;
Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAAAGCACTTGGCCACACTGATGCTCCGCTCTCCGCGCGCGCACTGGCGGA 60
DB 1 ATGAAAAGCACTTGGCCACACTGATGCTCCGCTCTCCGCGCGCGCACTGGCGGA 60
QY 61 GCGCATCCGGCTTTTACGTCGCAAGCGATGCGCACACGCAAAAGCCTCAAGCTCTTTA 120
DB 61 GCGCATCCGGCTTTTACGTCGCAAGCGATGCGCACACGCAAAAGCCTCAAGCTCTTTA 120
QY 121 GGTCTGCAAGAGCTTCAGCGCGGATCTCCGCGAGGCTACCGCATCAACGACCTCCGC 180
DB 121 GGTCTGCAAGAGCTTCAGCGCGGATCTCCGCGAGGCTACCGCATCAACGACCTCCGC 180
QY 181 TTGCGCGTCGATTACACGCGCTTACAAAATATATAAGCCCTTACCGATTTCAAACCTT 240
DB 181 TTGCGCGTCGATTACACGCGCTTACAAAATATATAAGCCCTTACCGATTTCAAACCTT 240
QY 241 TACAGCATCGCGCTCGCGCTTACGATTTACGATTCGACACCAATCCCGTCAACCGTAT 300
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QY 301 CTGCGCGCGCTTGGAGCTTCAACCGCGCTTCCGCGAGCTTGGCGGCGAGCAGCTTC 360
DB 301 CTGCGCGCGCTTGGAGCTTCAACCGCGCTTCCGCGAGCTTGGCGGCGAGCAGCTTC 360
QY 361 AGCCTTGGATCGCGCTTACCGCTTACGATTCGATTCGATTCGATTCGATTCGATTCG 420
DB 361 AGCCTTGGATCGCGCTTACCGCTTACGATTCGATTCGATTCGATTCGATTCGATTCG 420
QY 421 GTCCGTTCCGCGGAACCTGTCCGTCGGCGTGGCGCTCAAAATCTGA 525
DB 421 GTCCGTTCCGCGGAACCTGTCCGTCGGCGTGGCGCTCAAAATCTGA 525
RESULT 4
LOCUS CQ786532 525 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 1 from Patent WO2004019976.
ACCESSION CQ786532
VERSION CQ786532.1 GI:45721576
KEYWORDS Neisseria meningitidis
SOURCE

ORGANISM Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE 1
AUTHORS Martin, D. and Rioux, S.
TITLE Pharmaceutical liposomal compositions containing n. Meningitidis
derived polypeptides or polynucleotides
JOURNAL Patent: WO 2004019976-A 1 11-MAR-2004;
SHIRE BIOCHEM, INC. (CA)
FEATURES Location/Qualifiers
source 1..525
/organism="Neisseria meningitidis"
/mol_type="unassigned DNA"
/strain="608B"
/db_xref="taxon:487"
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Query Match 100.0%; Score 525; DB 6; Length 525;
Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAAAGCACTTGGCCACACTGATGCTCCGCTCTCCGCGCGCGCACTGGCGGA 60
DB 1 ATGAAAAGCACTTGGCCACACTGATGCTCCGCTCTCCGCGCGCGCACTGGCGGA 60
QY 61 GCGCATCCGGCTTTTACGTCGCAAGCGATGCGCACACGCAAAAGCCTCAAGCTCTTTA 120
DB 61 GCGCATCCGGCTTTTACGTCGCAAGCGATGCGCACACGCAAAAGCCTCAAGCTCTTTA 120
QY 121 GGTCTGCAAGAGCTTCAGCGCGGATCTCCGCGAGGCTACCGCATCAACGACCTCCGC 180
DB 121 GGTCTGCAAGAGCTTCAGCGCGGATCTCCGCGAGGCTACCGCATCAACGACCTCCGC 180
QY 181 TTGCGCGTCGATTACACGCGCTTACAAAATATATAAGCCCTTACCGATTTCAAACCTT 240
DB 181 TTGCGCGTCGATTACACGCGCTTACAAAATATATAAGCCCTTACCGATTTCAAACCTT 240
QY 241 TACAGCATCGCGCTCGCGCTTACGATTTACGATTCGACACCAATCCCGTCAACCGTAT 300
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DB 301 CTGCGCGCGCTTGGAGCTTCAACCGCGCTTCCGCGAGCTTGGCGGCGAGCAGCTTC 360
QY 361 AGCCTTGGATCGCGCTTACCGCTTACGATTCGATTCGATTCGATTCGATTCGATTCG 420
DB 361 AGCCTTGGATCGCGCTTACCGCTTACGATTCGATTCGATTCGATTCGATTCGATTCG 420
QY 421 GTCCGTTCCGCGGAACCTGTCCGTCGGCGTGGCGCTCAAAATCTGA 525
DB 421 GTCCGTTCCGCGGAACCTGTCCGTCGGCGTGGCGCTCAAAATCTGA 525
RESULT 5
LOCUS CQ814512 525 bp DNA linear PAT 24-MAY-2004
DEFINITION Sequence 8 from Patent WO2004020452.
ACCESSION CQ814512
VERSION CQ814512.1 GI:47603711
KEYWORDS Neisseria meningitidis
ORGANISM Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE 1
AUTHORS Biemans, R., Bos, M., Dencel, P., Peron, C., Goraj, K., Poolman, J.,
Tomassen, J. and Weynants, V.
TITLE Refolding method

JOURNAL Patent: WO 2004020452-A 8 11-MAR-2004;
GlaxoSmithKline Biologics S.A. (BE); Utrecht University (NL)

FEATURES
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1.525
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/mol_type="unassigned DNA"
/db_xref="taxon:487"

ORIGIN

Query Match 100.0%; Score 525; DB 6; Length 525;
Best Local Similarity 100.0%; Pred. No. 1.1e-89;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAAAGACATTTGCCACACTGATTCCTCGCTCTCCGGCGCGCGCACTGCGCGAA 60
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Qy 61 GGCGATCCGGCTTTAGCTCAAGCGCATGCGGACACGCAAGAGCTCAAGCTCTTTA 120
Db 61 GGCGATCCGGCTTTAGCTCAAGCGCATGCGGACACGCAAGAGCTCAAGCTCTTTA 120

Qy 121 GGTTCGCAAGGCTTCAGCGCGCGCATCTCCGAGGCTACCGCATCAACGACCTCGC 180
Db 121 GGTTCGCAAGGCTTCAGCGCGCGCATCTCCGAGGCTACCGCATCAACGACCTCGC 180

Qy 181 TTGCGCGTTCGATTAACGCGCTTACAAACATATAAGCCCATCCACGATTTCAAACTT 240
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Qy 241 TACAGCATCGCGGCTCGCCATTTAGACTTCGACACCCCAATCGCCGTCAAAACCGTAT 300
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Qy 301 CTGCGCGCGCTTGAGCTCAACGCGGCTCGCTCGACTTTGGGCGGCGACGAGCTTC 360
Db 301 CTGCGCGCGCTTGAGCTCAACGCGGCTCGCTCGACTTTGGGCGGCGACGAGCTTC 360

Qy 361 AGCCAAACTTCATCGGCTCGGCTATTAGCGGCGTAAAGCTATGCGGTTACCCGAAAT 420
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Qy 421 GTCGATTTGGATCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 480
Db 421 GTCGATTTGGATCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 480

Qy 481 GTCCGTTCCGCGCAACTGTCGCTCGGCGTCAAAATTTCTGA 525
Db 481 GTCCGTTCCGCGCAACTGTCGCTCGGCGTCAAAATTTCTGA 525

RESULT 6
NMU52066
LOCUS NMU52066 830 bp DNA linear BCT 03-SEP-1999
DEFINITION Neisseria meningitidis outer membrane protein gene, complete cds.
ACCESSION U52066
VERSION U52066.1 GI:1518521
KEYWORDS
SOURCE Neisseria meningitidis
ORGANISM Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
AUTHORS 1 (bases 1 to 830)
TITLE Martin, D., Cadieux, N., Hamel, J., and Brodeur, B.R.
Highly conserved Neisseria meningitidis surface protein confers protection against experimental infection
J. Exp. Med. 185 (7), 1173-1183 (1997)
JOURNAL 9104804
PUBMED
REFERENCE 2 (bases 1 to 830)
AUTHORS Plante, M., Cadieux, N., Rioux, C.R., Hamel, J., Brodeur, B.R. and Martin, D.
TITLE Antigenic and molecular conservation of the gonococcal NspA protein
JOURNAL Infect. Immun. 67 (6), 2855-2861 (1999)
PUBMED 10338491

REFERENCE 3 (bases 1 to 830)
AUTHORS Cadieux, N., Plante, M., Rioux, C.R., Hamel, J., Brodeur, B.R. and Martin, D.
TITLE Bactericidal and cross-protective activities of a monoclonal antibody directed against Neisseria meningitidis NspA outer membrane protein
Infect. Immun. 67 (9), 4955-4959 (1999)
JOURNAL 10456958
PUBMED
REFERENCE 4 (bases 1 to 830)
AUTHORS Martin, D.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-1996) Denis Martin, Department of Microbiology, University Laval, Unite de Vaccinologie, Laboratoire et Service d'Infectiologie, Centre Hospitalier de l'Universite Laval, 2705 boul Laurier, Ste-Foy, Quebec G1V 4G2, Canada
Location/Qualifiers
FEATURES
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Best Local Similarity 100.0%; Pred. No. 1.1e-89;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 GGCGATCCGGCTTTAGCTCAAGCGCATGCGGACACGCAAGAGCTCAAGCTCTTTA 120
Db 203 GGCGATCCGGCTTTAGCTCAAGCGCATGCGGACACGCAAGAGCTCAAGCTCTTTA 262

Qy 121 GGTTCGCAAGGCTTCAGCGCGCGCATCTCCGAGGCTACCGCATCAACGACCTCGC 180
Db 263 GGTTCGCAAGGCTTCAGCGCGCGCATCTCCGAGGCTACCGCATCAACGACCTCGC 322

Qy 181 TTGCGCGTTCGATTAACGCGCTACAAACATATAAGCCCATCCACGATTTCAAACTT 240
Db 323 TTGCGCGTTCGATTAACGCGCTACAAACATATAAGCCCATCCACGATTTCAAACTT 382

Qy 241 TACAGCATCGCGGCTCGGCTTTAGACTTCGACACCCCAATCGCCGTCAAAACCGTAT 300
Db 383 TACAGCATCGCGGCTCGGCTTTAGACTTCGACACCCCAATCGCCGTCAAAACCGTAT 442

Qy 301 CTGCGCGCGCTTGAGCTCAACGCGGCTTCGCTCGACTTTGGGCGGCGACGAGCTTC 360
Db 443 CTGCGCGCGCTTGAGCTCAACGCGGCTTCGCTCGACTTTGGGCGGCGACGAGCTTC 502

Qy 361 AGCCAAACTTCATCGGCTCGGCTATTAGCGGCGGCTAAGCTATGCGGTTACCCGAAAT 420
Db 503 AGCCAAACTTCATCGGCTCGGCTATTAGCGGCGGCTAAGCTATGCGGTTACCCGAAAT 562

Qy 421 GTCGATTTGGATCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 480
Db 563 GTCGATTTGGATCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 622

QY 481 GTCCGTTCCGGCAACTGTCCTCGCGGTGCGCGTCAAAATTCGA 525
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Db 623 GTCCGTTCCGGCAACTGTCCTCGCGGTGCGCGTCAAAATTCGA 667

RESULT 7

LOCUS AR167414 AR167414 830 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6287574.
ACCESSION AR167414
VERSION AR167414.1 GI:17903193
KEYWORDS
SOURCE Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 830)

AUTHORS Brodeur, B.R., Martin, D., Hamel, J. and Rioux, C.

TITLE Proteinase K resistant surface-protein of neisseria meningitidis

JOURNAL Patent: US 6287574-A 1 11-SEP-2001;

FEATURES Location/Qualifiers

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/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 525; DB 6; Length 830;
Best Local Similarity 100.0%; Pred. No. 1.1e-89;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCACTTGCACACTGATGGCTTCGCTCTCCGGCGCGCGCACTGGCGGAA 60
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QY 61 GGCGCATCCGGCTTTTACGTCAAGCCGATGCGGCACACGCAAAAGCTCAAGCTCTTTA 120
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QY 121 GGTTCGCAAGGCTTCAAGCCGCGATCTCCGAGGCTACCGCATCAAGCACTTCGCG 180
Db 263 GGTTCGCAAGGCTTCAAGCCGCGATCTCCGAGGCTACCGCATCAAGCACTTCGCG 322
QY 181 TTCCGCGTCAATACCGCGGTACAAATATATAAGCCGATCCACGATTTCAAACTT 240
Db 323 TTCCGCGTCAATACCGCGGTACAAATATATAAGCCGATCCACGATTTCAAACTT 382
QY 241 TACAGCATCGCGGTTCGCGCATTTACGACTTCGACACCCCAATCCCGTCAAAACGAT 300
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QY 361 AGCCAAACTTCATCGGCTCGGCTATGAGCGGCTAAGCTATGCGGTACCCCGAAT 420
Db 503 AGCCAAACTTCATCGGCTCGGCTATGAGCGGCTAAGCTATGCGGTACCCCGAAT 562
QY 421 GTCGATTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480
Db 563 GTCGATTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 622
QY 481 GTCCGTTCCGGCAACTGTCCTCGCGGTGCGCGTCAAAATTCGA 525
Db 623 GTCCGTTCCGGCAACTGTCCTCGCGGTGCGCGTCAAAATTCGA 667

RESULT 8

LOCUS AF175678 AF175678 525 bp DNA linear BCT 06-SEP-1999
DEFINITION Neisseria meningitidis strain CU385 surface protein A (nspA) gene,
complete cds.
ACCESSION AF175678
VERSION AF175678.1 GI:5825530

KEYWORDS

SOURCE

ORGANISM

Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

Location/Qualifiers

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/organism="Neisseria meningitidis"

/mol_type="genomic DNA"

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/db_xref="taxon:487"

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1..525

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ORIGIN

Query Match 99.4%; Score 521.8; DB 1; Length 525;

Best Local Similarity 99.6%; Pred. No. 4.7e-89;

Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 61 GGCGCATCCGGCTTTTACGTCAAGCCGATGCGGCACACGCAAAAGCTCAAGCTCTTTA 120
QY 121 GGTTCGCAAGGCTTCAAGCCGCTCCGTCGACTTGGGCGGAGGACAGCTTC 180
Db 121 GGTTCGCAAGGCTTCAAGCCGCTCCGTCGACTTGGGCGGAGGACAGCTTC 180
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Db 181 TTCCGCGTCAATACCGCGGTACAAATATATAAGCCGATCCACGATTTCAAACTT 240
QY 241 TACAGCATCGCGGTTCGCGCATTTACGACTTCGACACCCCAATCCCGTCAAAACGAT 300
Db 241 TACAGCATCGCGGTTCGCGCATTTACGACTTCGACACCCCAATCCCGTCAAAACGAT 300
QY 301 CTCGCGCGCGCTTGAGGCTTCAAGCCGCTCCGTCGACTTGGGCGGAGGACAGCTTC 360
Db 301 CTCGCGCGCGCTTGAGGCTTCAAGCCGCTCCGTCGACTTGGGCGGAGGACAGCTTC 360
QY 361 AGCCAAACTTCATCGGCTCGGCTATGAGCGGCTAAGCTATGCGGTACCCCGAAT 420
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QY 421 GTCGATTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480
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QY 481 GTCCGTTCCGGCAACTGTCCTCGCGGTGCGCGTCAAAATTCGA 525

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Db 481 GTCCGTTCCGCGCAACTGTCCGCGGTGTGCGCGTCAAAATCTGA 525
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Query Match 99.4%; Score 521.8; DB 1; Length 110000;
Best Local Similarity 99.6%; Pred. No. 3e-89;
Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGAAAAGACATTGGCACACTGATTCGCTCCGCGCGCGCGCACTGGCGGAA 60
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Qy 121 GGTTCGCAAGGCTTCAGCCCGCGGATCTCCGAGGCTACCGATCAACGACCTCCGC 180
Db 90702 GGTTCGCAAGGCTTCAGCCCGCGGATCTCCGAGGCTACCGATCAACGACCTCCGC 90643
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Qy 181 TTCGCGTTCGATTACAGCGCTACAAAACCTATAAGCCCATCCACCGATTTCAAACTT 240
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Qy 301 CTCGCGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTGGGCGGAGCGACAGCTTC 360
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Qy 421 GTCCGATTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 480
Db 90402 GTCCGATTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 90343
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RESULT 10

AX044030/c 349980 bp DNA linear PAT 24-NOV-2000
LOCUS Sequence 109 from Patent WO0066791.

AX044030
ACCESSION

AX044030.1 GI:11342914

KEYWORDS

Neisseria meningitidis

ORGANISM

Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.

REFERENCE

AUTHORS

Pizza, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J. C.,
Maignani, V., Galeotti, C., Mora, M., Ratti, G., Scarselli, M.,
Scariato, V., Rappuoli, R., Frazer, C. M. and Grandi, G.
Neisseria genomic sequences and methods of their use
Patent: WO 0066791-A 109 09-NOV-2000;

TITLE

JOURNAL

CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)

FEATURES

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seq 109: 600001 to 949980 349980 bases
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seq 113: 1800001 to 2149980 349980 bases
seq 114: 2100001 to 2272325 172325 bases"

ORIGIN

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Best Local Similarity 99.6%; Pred. No. 2.7e-89;
Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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RESULT 11

NM52068

LOCUS NM52068 850 bp DNA linear BCT 03-SEP-1999

DEFINITION Neisseria meningitidis outer membrane protein gene, complete cds.

ACCESSION U52068

VERSION U52068.1 GI:1808966

KEYWORDS

SOURCE Neisseria meningitidis

ORGANISM Neisseria meningitidis

REFERENCE 1 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.

AUTHORS Cadieux,N., Plante,M., Rioux,C.R., Hamel,J., Brodeur,B.R. and Martin,D. (bases 1 to 850)

TITLE Bactericidal and cross-protective activities of a monoclonal antibody directed against Neisseria meningitidis NspA outer membrane protein

JOURNAL Infect. Immun. 67 (9), 4955-4959 (1999)

PUBMED 10456958

REFERENCE 2 (bases 1 to 850)

AUTHORS Martin,D.

TITLE Direct Submission

JOURNAL Submitted (22-MAR-1996) Denis Martin, Department of Microbiology, University Laval, Unite de Vaccinologie, Laboratoire et Service d'Infectiologie, Centre Hospitalier de l'Universite Laval, 2705 boul Laurier, Ste-Foy, Quebec G1V 4G2, Canada

FEATURES

source Location/Qualifiers

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sig_peptide 208..264

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Best Local Similarity 99.2%; Pred. No. 1.8e-88;

Matches 521; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 328 GGTTCGCAAGGCTTCAGCGCGCGCATCTCCGAGGCTACCGCATCAAGCCTCCGC 387

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RESULT 12

AR167416

LOCUS AR167416 850 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 5 from patent US 6287574.

ACCESSION AR167416

VERSION AR167416.1 GI:17903195

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 850)

AUTHORS Brodeur,B.R., Martin,D., Hamel,J. and Rioux,C.

TITLE Proteinase K resistant surface protein of neisseria meningitidis

JOURNAL Patent: US 6287574-A 5 11-SEP-2001;

FEATURES

source Location/Qualifiers

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/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 98.8%; Score 518.6; DB 6; Length 850;

Best Local Similarity 99.2%; Pred. No. 1.8e-88;

Matches 521; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 208 ATGAAAAAGCACTTGCACACTGATTCGCCCTCGCTCTCCGGCGCGCGCACTGGCGGAA 267

Qy 61 GCGCATCCGGCTTTTACGTCCAAAGCGATGCGGACACGCAAAAGCCTCAAGCTCTTTA 120

Db 268 GCGCATCCGGCTTTTACGTCCAAAGCGATGCGGACACGCAAAAGCCTCAAGCTCTTTA 327

Qy 121 GGTTCGCAAGGCTTCAGCGCGCGCATCTCCGAGGCTACCGCATCAAGCCTCCGC 180

Db 328 GGTTCGCAAGGCTTCAGCGCGCGCATCTCCGAGGCTACCGCATCAAGCCTCCGC 387

Qy 181 TTCCGCGTGCATTTACGTCCAAAGCGATGCGGACACGCAAAAGCCTCAAGCTCTTTA 240

Db 388 TTCCGCGTGCATTTACGTCCAAAGCGATGCGGACACGCAAAAGCCTCAAGCTCTTTA 447

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Qy 301 CTCCGGCGCGCTTCAGCTCAACCGCGCTTCGGTTCGACTTTGGGCGGCGAGCAGCTTC 360

Db 508 CTCCGGCGCGCTTCAGCTCAACCGCGCTTCGGTTCGACTTTGGGCGGCGAGCAGCTTC 567

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fasta scores; E(): 5.1e-32, 58.0% identity in 138 aa
overlap. Shows very weak similarity to eukaryotic
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Query Match 98.8%; Score 518.6; DB 1; Length 311321;
Best Local Similarity 99.2%; Pred. No. 1.1e-88;
Matches 521; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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LOCUS AF175677
DEFINITION Neisseria meningitidis strain BZ232 surface protein A (nsa) gene,
complete cds.
ACCESSION AF175677
VERSION AF175677.1 GI:5825528
KEYWORDS Neisseria meningitidis
SOURCE Neisseria meningitidis
ORGANISM Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 525)
Moe, G.R., Tan, S. and Granoff, D.M.
Differences in Surface Expression of Neisserial Surface Protein A
among Neisseria meningitidis Group B strains
Infect. Immun. (1999) In press
JOURNAL REFERENCE 2 (bases 1 to 525)
Moe, G.R., Tan, S. and Granoff, D.M.
Direct Submission
AUTHORS Submitted (04-AUG-1999) Children's Hospital Oakland Research
Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
JOURNAL Location/Qualifiers
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2006, 18:34:18 ; Search time 492 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues
Total number of hits satisfying chosen parameters: 9993994

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	525	100.0	830	8	ACA64711 N. mening
5	525	100.0	830	10	ADF43315 N. mening
6	525	100.0	830	14	AEA03009 Neisseria
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8	521.8	99.4	110000	3	AAA81490.06
9	521.8	99.4	349980	3	AAT21608 Neisseria
10	518.6	98.8	850	2	AAT39041 Proteinas
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14	480.2	91.5	525	10	ABZ38961 N. gonorr
15	464.8	88.5	468	12	ADL13425 Neisseria
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ALIGNMENTS

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AC ADL13427;	
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DT 03-JUN-2004 (first entry)	
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DE Neisseria meningitidis H44/76 NspA gene.	
XX	
KW Neisserial surface protein A; NspA; refolding; recombinant production;	
KW vaccine; subunit vaccine; prevention; diagnosis; meningococcus;	
KW invasive bacterial disease; bacteraemia; meningitis;	
KW Neisseria gonorrhoeae; gonorrhoea; mature protein; strain H44/76;	
KW antibacterial; gene therapy; gene; da.	
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OS Neisseria meningitidis; H44/76.	
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WO2004020452-A2.

11-MAR-2004.

28-AUG-2003; 2003WO-EP010085.

30-AUG-2002; 2002GB-00020197.

(GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
(UUT-) RIJKSUNIV UTRECHT.

XX Biemans R, Bos M, Dencel P, Feron C, Goraj K, Poolman J;
PI Tommaassen J, Weynants V;

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DT	16-OCT-2003 (revised)
DT	22-DEC-1996 (first entry)
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XX	
KW	Proteinase K resistant; <i>Neisseria meningitidis</i> ; <i>Neisseria g</i>
KW	antibody; detection; probe; surface protein; ss.

DE Proteinase K resistant N. meningitidis 22 kD surface protein.

Proteinase K resistant; *Neisseria meningitidis*; *Neisseria gonorrhoeae*; KW antibody; detection; probe; surface protein; ss. KW

XX
OS
OS

Key	Location/Qualifiers
-10_signal	75..80
FT	/*tag= d
FT	
FT	
FT	131..135
RBS	
FT	/*tag= e
FT	143..667
CDS	
FT	/*tag= a
FT	143..199
sig_peptide	
FT	/*tag= b
FT	200..664
mat_peptide	
FT	/*tag= c
FT	
FT	

WO9629412-A1

XX
PD 26-SEP-1996.

XX
PF 15-MAR-1996; 96WO-CA000157.

XX
PR 17-MAR-1995; 95US-00406362.

PR 04-AUG-1995; 95US-0001983P.
XX

PA (IAFB-) IAF BIO VAC INC.
XX

PI Brodeur BR, Martin D, Hamel J, Rioux C;

XX
np
WPT: 1996-443187/44

DR P-PSDB; AAW04891.

XX	PT	PT	XX	PS	XX	CC	CC	CC	CC	CC	CC	CC	CC	XX	SQ	QY	Db	QY	Db	QY	Db	QY	Db	QY	Db	QY	Db	QY	Db	QY	Db	REES	AC	ID	XX	AC	XX	DT	XX	DE	XX	KW	KW	KW
----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	------	----	----	----	----	----	----	----	----	----	----	----	----

Neisseria meningitidis antigen, highly conserved strains - useful for prodn. of antibodies for imm diagnosis of, N. meningitidis infection.

Claim 12; Fig 1; 117pp; English.

A proteinase K resistant surface protein has been identified in *N. meningitidis* (AAR3939 to AAR39042). The immunogenic fragments of antibodies can be used in the prevention of infection by *N. meningitidis* or by humans. The antibodies may also be used diagnostically in meningitis infection. The antigen may also be used specific to *N. meningitidis* infection. DNA sequences specific to *N. meningitidis* antigen can be used as probes for the detection of the antigen in their fragments, can be used as probes for the detection of *N. meningitidis* bacteria. (Updated on 16-OCT-2003 to the Neisseria bacteria.)

Sequence 830 BP: 210 A; 261 C; 175 G; 184 T; 0 U; 0 Other;

```
Query Match      100.0%; Score 525; DB 2; Length 830;
Best Local Similarity 100.0%; Pred. No. 5.9e-125;
Matches 525; Conservative 0; Mismatches 0; Indels
```

1	ATGAAAAAGCACTTGCCACACTGATGGCCCTCGCTCTCCCGCGCGCGCACTGGCGGAA	60
143	ATGAAAAAGCACTTGCCACACTGATGGCCCTCGCTCTCCCGCGCGCGCACTGGCGGAA	202
61	GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCAACGCAAAAGGCTCTTTTA	120
203	GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCAACGCAAAAGGCTCTTTTA	262
121	GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAAGGCTACCGCACTCAACGACCTCCGC	180
263	GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAAGGCTACCGCACTCAACGACCTCCGC	322
181	TTCCGCGCTGATTAACGCGCTACAAAAAATAAAGAGCCCATCCACCGATTTCAAACTT	240
323	TTCCGCGCTGATTAACGCGCTACAAAAAATAAAGAGCCCATCCACCGATTTCAAACTT	382
241	TACAGCATCGGCGCTCGGCACTTACGACTTCGACACCCAAATGCGCCGTCAAACCGTAT	300
383	TACAGCATCGGCGCTCGGCACTTACGACTTCGACACCCAAATGCGCCGTCAAACCGTAT	442
301	CTCGGCGCGGCTTGAGCCTCAACCGGCGCTCCGTGCACTTGGCGCGCAGCAGCTTC	360
443	CTCGGCGCGGCTTGAGCCTCAACCGGCGCTCCGTGCACTTGGCGCGCAGCAGCTTC	502
361	AGCCAAACTCCATATCGGCTTCGGCGTATTGACGGGGTAAAGCTATGCGGTACCCCGAAT	420
503	AGCCAAACTCCATATCGGCTTCGGCGTATTGACGGGGTAAAGCTATGCGGTACCCCGAAT	562
421	GTGCAATTTGGATGCCGGCTACCGCTACAACTATATCGGCAAAGTCAACACTGTCAAAAC	480
563	GTGCAATTTGGATGCCGGCTACCGCTACAACTATATCGGCAAAGTCAACACTGTCAAAAC	622
481	GTCCGTTCCGGGAACTGCCGCTGCGCGTCAAAATTTGA	525
623	GTCCGTTCCGGGAACTGCCGCTGCGCGTCAAAATTTCTGA	667

RESULT 4

ACA64711

ID ACA64711 standard; DNA: 830 BP.

ACA
ACA64711;

XX DT 18-JUN-2003 (first entry)

XX DE *N. meningitidis* lipopolysaccharide gene.

Superantigen; ds; gene; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis; gene therapy; mammalian cell receptor; cytostatic; tumour associated lipid; energy; T cell; antigen presenting cell; APC;

4462
+ 2221
2221

KW tumouricidal immunocyte; antitumour.

OS Neisseria meningitidis.

XX US2002177551-A1.

XX 28-NOV-2002.

XX 30-MAY-2001; 2001US-00870759.

XX 31-MAY-2000; 2000US-0208128P.

XX (TERM/) TERMAN D S.

XX Terman DS;

XX WPI; 2003-361759/34.

XX P-PSDB; ABU79079.

XX A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces energy or apoptosis in T cells and antigen presenting cells.

XX Disclosure; Page; 167pp; English.

The invention relates to a mammalian cell receptor, useful in the treatment of cancer, which binds to tumor associated lipids and induces energy or apoptosis in the T cells and antigen presenting cells (APCs). Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumor associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (M1) a tumouricidal immunocyte population in vivo in a mammal by allowing tumor associated lipids to contact immunocytes in which receptors for immunosuppressive fatty acids, ceramides, glycolipids, sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides, sialylated glycans, lipopeptides and proteoglycolipids are inactivated or deleted), a construct useful in the treatment of cancer comprising a superantigen (Sag) nucleotide inserted into a virus, a mammalian T cell useful in the treatment of cancer (where an adaptor protein which inhibits T cell activation by tumor associated antigens is deleted or functionally deactivated), a composition useful in the treatment of cancer (comprising a lipid raft conjugated to a superantigen), producing (M2) a tumouricidal immunocyte population ex vivo in a mammal (by allowing tumor associated lipids to contact immunocytes, in which receptors for the lipids are inactivated or deleted to produce a tumouricidal immunocyte population, and administering the tumouricidal APCs to the host), producing a tumouricidal T cell population ex vivo in a mammal by allowing a tumour associated lipid to contact T cells, in which adaptor proteins, which inhibit T cell activation by tumor associated antigens, are deleted or functionally deactivated to produce a tumouricidal population of T cells, and administering the tumouricidally activated T cells to the host, or allowing a superantigen-lipid raft to contact T cells ex vivo, and administering the tumouricidally activated T cells to the host), treating (M5) cancer in a mammal (by administering a lipid binding molecule which binds immunosuppressive tumor associated lipids in vivo), producing (M6) a tumouricidal T cell population in vivo in a mammal (by allowing a tumour associated antigen to contact immunocytes in which adaptor proteins which inhibit T cell activation by tumor associated antigens are deleted or functionally deactivated) and producing (M7) a tumouricidal T cell population ex vivo in a mammal comprising allowing a superantigen-lipid raft conjugate to contact immunocytes in vivo. The receptors, methods and compositions are useful for treating cancers and tumours. Bacterial superantigens are co-administered or administered as fusion constructs with anti-tumour proteins or motifs. The present sequence encodes an anti-tumour protein which is co-administered with or incorporated into a fusion construct with a superantigen. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from the US patent

CC office website at "seqdata.uspto.gov/sequence.html?DocID=2002177551"

XX Sequence 830 BP; 210 A; 261 C; 175 G; 184 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 525; DB 8; Length 830;

Best Local Similarity 100.0%; Pred. No. 5.9e-125;

Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCAGCTTGGCACAATGATGCGCTCGCTCTCCGGCGCGCGCAGCTCGCGGAA 60

DB 143 ATGAAAAAGCAGCTTGGCACAATGATGCGCTCGCTCTCCGGCGCGCGCAGCTCGCGGAA 202

QY 61 GGCGCATCCGGCTTTTACGTCCCAAGCGGATGCGCGCACACGCAAAAGCTCAAGCTCTTTA 120

DB 203 GGCGCATCCGGCTTTTACGTCCCAAGCGGATGCGCGCACACGCAAAAGCTCAAGCTCTTTA 262

QY 121 GGTTCTGCCAAAGCTTACGCGCGCGCATCTCCGCGGCTACCGCATCAAGCAGCTCGGC 180

DB 263 GGTTCTGCCAAAGCTTACGCGCGCGCATCTCCGCGGCTACCGCATCAAGCAGCTCGGC 322

QY 181 TTGCGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240

DB 323 TTGCGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 382

QY 241 TACAGCATCGCGCGCTCGCGCATTTACGATTTGACGATTTGACGATTTGACGATTTGACGAT 300

DB 383 TACAGCATCGCGCGCTCGCGCATTTACGATTTGACGATTTGACGATTTGACGATTTGACGAT 442

QY 301 CTGCGCGCGCTTGGAGCTTACCGCGCTTACCGCGCTTACCGCGCTTACCGCGCTTACCGCGCT 360

DB 443 CTGCGCGCGCTTGGAGCTTACCGCGCTTACCGCGCTTACCGCGCTTACCGCGCTTACCGCGCT 502

QY 361 AGCCAAACCTCCATCGCGCTCGCGCTTACGATTTGACGATTTGACGATTTGACGATTTGACGAT 420

DB 503 AGCCAAACCTCCATCGCGCTCGCGCTTACGATTTGACGATTTGACGATTTGACGATTTGACGAT 562

QY 421 GTGATTTGGATCGCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCG 480

DB 563 GTGATTTGGATCGCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCG 622

QY 481 GTGATTTGGATCGCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCG 525

DB 623 GTGATTTGGATCGCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCG 667

RESULT 5

ADP43315

ID ADP43315 standard; DNA; 830 BP.

XX

AC ADP43315;

XX

DT 12-FEB-2004 (first entry)

XX

DE N. meningitidis lipopolysaccharide DNA seq id 35.

XX

KW receptor; lipid-based tumour associated antigen; cytostatic;

KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;

KW infectious disease; lipopolysaccharide; LPS; ds.

OS

OS Neisseria meningitidis.

PN US2003157413-A1.

XX 21-AUG-2003.

XX

PF 28-DEC-2000; 2000US-00751708.

XX

PR 28-DEC-1999; 99US-0173371P.

XX

PA (TERM/) TERMAN D S.

XX

PI Terman DS;

XX

DR WPI; 2003-787326/74.
XX P-PSDB; ADF43316.
XX
PT New receptor in a mammalian cell that inhibits regular activation by
PT receptors specific for lipid-based tumor associated antigens, useful for
PT treating a neoplastic disease or tumor, and infectious diseases.
XX
XX
PS Disclosure; SEQ ID NO 35; 151pp; English.
XX
XX The invention describes a receptor in a mammalian cell that inhibits
CC regular activation by receptors specific for lipid-based tumor
CC associated antigen. The receptor has cytostatic and antimicrobial
CC properties and is suitable for use in gene therapy. The receptors,
CC methods and compositions are useful for treating a neoplastic disease or
CC tumor (cancer), and infectious diseases. This sequence encodes *Neisseria*
CC meningitidis lipopolysaccharide (LPS) to which tumor cells develop
CC immunity.
XX
SQ Sequence 830 BP; 210 A; 261 C; 175 G; 184 T; 0 U; 0 Other;
Query Match 100.0%; Score 525; DB 10; Length 830;
Best Local Similarity 100.0%; Pred. No. 5.9e-125;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAAAAAGCACTTGCACACTGATGGCTCTCCGGCCGCGCACTGGCGGAA 60
Db 143 ATGAAAAAGCACTTGCACACTGATGGCTCTCCGGCCGCGCACTGGCGGAA 202
Qy 61 GGCGCATCCGGCTTTTACGTCCAGCGATGCGGCACACGCAAGAGCTCAAGCTCTTTA 120
Db 203 GGCGCATCCGGCTTTTACGTCCAGCGATGCGGCACACGCAAGAGCTCAAGCTCTTTA 262
Qy 121 GGTTCGTGCAAAAGGCTTCAGCGCGCATCTCCGAGGCTACCGCATCAAGCACTTCGCG 180
Db 263 GGTTCGTGCAAAAGGCTTCAGCGCGCATCTCCGAGGCTACCGCATCAAGCACTTCGCG 322
Qy 181 TTCGCGGTGCAATACACGCGCTACAAAACATATAAGCCCATCCACGATTTCAAACCTT 240
Db 323 TTCGCGGTGCAATACACGCGCTACAAAACATATAAGCCCATCCACGATTTCAAACCTT 382
Qy 241 TACAGCATCGGGCGTTCGCCATTTACACTTCGACACCCATCGCCGTCARACCGTAT 300
Db 383 TACAGCATCGGGCGTTCGCCATTTACACTTCGACACCCATCGCCGTCARACCGTAT 442
Qy 301 CTCGGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTGGGCGGAGCAGAGCTTC 360
Db 443 CTCGGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTGGGCGGAGCAGAGCTTC 502
Qy 361 AGCCAAACCTCCATCGGCTCGGGTATTTGACGGGCGTAAGCTATGCCGTTACCCCGAAT 420
Db 503 AGCCAAACCTCCATCGGCTCGGGTATTTGACGGGCGTAAGCTATGCCGTTACCCCGAAT 562
Qy 421 GTCGATTTGGATCGCGGTACCGGTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 480
Db 563 GTCGATTTGGATCGCGGTACCGGTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 622
Qy 481 GTCCGCTTCGGGCAACTGTCCGTCGGCGTGGCGTCAAAATTTCTGA 525
Db 623 GTCCGCTTCGGGCAACTGTCCGTCGGCGTGGCGTCAAAATTTCTGA 667
RESULT 6
ID AEA03009 standard; DNA; 830 BP.
XX
AC AEA03009;
XX
XX 28-JUL-2005 (first entry)
XX DE *Neisseria meningitidis* meningococcal meningitis DNA SEQ ID NO:35.
XX
XX tumor; neoplasm; gene therapy; immunotherapy; cytostatic; meningitis;
KW gene; ds.

XX *Neisseria meningitidis*.
XX OS
XX PN US2005112141-A1.
XX
XX PD 26-MAY-2005.
XX
XX PF 08-SEP-2004; 2004US-00937758.
XX
XX PR 30-AUG-2000; 2000US-00650884.
XX
XX PA (TERM/) TERMAN D S.
XX
XX PI Terman DS;
XX
XX DR WPI; 2005-394926/40.
XX P-PSDB; AEA03010.
XX
XX New composition for treating a tumor or neoplastic disease in a subject
XX comprises conjugates comprising superantigen polypeptides or nucleic
XX acids with other molecules that produce a tumoricidal response.
XX
XX Disclosure; SEQ ID NO 35; 125pp; English.
XX
XX The invention relates to a composition for treating a tumor or neoplastic
XX disease in a subject. Also described: (1) a mammalian cell comprising an
XX exogenous nucleic acid encoding a superantigen expressed in the cell,
XX which cell also produces or expresses all alpha-anomers of
XX monoglycosylceramide or diglycosylceramide, where expression of the
XX superantigen and the mono- or diglycosylceramide is capable of eliciting
XX an antitumor immune response in a mammal into which the cell is
XX introduced; (2) treating a tumor or neoplastic disease in a subject; (3)
XX preparing a population of immunotherapeutic T or natural killer T (NKT)
XX cells useful to treat a tumor or neoplastic disease in a subject; (4) an
XX apoptotic cell preparation or lysate useful for treating a tumor or
XX neoplastic disease in a subject, comprising a cell population that has
XX been transfected with naked DNA encoding a superantigen, and treated to
XX undergo apoptosis or lysis; and (5) a cell that has ingested or been
XX transfected with the above apoptotic preparation or lysate, thus,
XX rendering the cell effective in presenting material expressed from
XX a transfecting nucleic acid or material ingested to the immune system of a
XX mammal to elicit an anti-tumor immune response. The composition and
XX methods are useful for treating tumors or neoplastic diseases. The
XX present sequence represents a *Neisseria meningitidis* nucleotide sequence
XX which induces meningococcal meningitis, which is given in the
XX exemplification of the present invention. Note - The sequence data for
XX this patent is not represented in the printed specification, but was
XX obtained in electronic format directly from the USPTO web site.
XX
SQ Sequence 830 BP; 210 A; 261 C; 175 G; 184 T; 0 U; 0 Other;
Query Match 100.0%; Score 525; DB 14; Length 830;
Best Local Similarity 100.0%; Pred. No. 5.9e-125;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAAAAAGCACTTGCACACTGATGGCTCTCCGGCCGCGCACTGGCGGAA 60
Db 143 ATGAAAAAGCACTTGCACACTGATGGCTCTCCGGCCGCGCACTGGCGGAA 202
Qy 61 GGCGCATCCGGCTTTTACGTCCAGCGCATGCGGCACACGCAAGAGCTCAAGCTCTTTA 120
Db 203 GGCGCATCCGGCTTTTACGTCCAGCGCATGCGGCACACGCAAGAGCTCAAGCTCTTTA 262
Qy 121 GGTTCGTGCAAAAGGCTTCAGCGCGCATCTCCGAGGCTACCGCATCAAGCACTTCGCG 180
Db 263 GGTTCGTGCAAAAGGCTTCAGCGCGCATCTCCGAGGCTACCGCATCAAGCACTTCGCG 322
Qy 181 TTCGCGGTGCAATACACGCGCTACAAAACATATAAGCCCATCCACGATTTCAAACCTT 240
Db 323 TTCGCGGTGCAATACACGCGCTACAAAACATATAAGCCCATCCACGATTTCAAACCTT 382
Qy 241 TACAGCATCGGGCGTTCGCCATTTACACTTCGACACCCATCGCCGTCARACCGTAT 300
Db 383 TACAGCATCGGGCGTTCGCCATTTACACTTCGACACCCATCGCCGTCARACCGTAT 442
Qy 301 CTCGGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTGGGCGGAGCAGAGCTTC 360
Db 443 CTCGGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTGGGCGGAGCAGAGCTTC 502
Qy 361 AGCCAAACCTCCATCGGCTCGGGTATTTGACGGGCGTAAGCTATGCCGTTACCCCGAAT 420
Db 503 AGCCAAACCTCCATCGGCTCGGGTATTTGACGGGCGTAAGCTATGCCGTTACCCCGAAT 562
Qy 421 GTCGATTTGGATCGCGGTACCGGTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 480
Db 563 GTCGATTTGGATCGCGGTACCGGTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 622
Qy 481 GTCCGCTTCGGGCAACTGTCCGTCGGCGTGGCGTCAAAATTTCTGA 525
Db 623 GTCCGCTTCGGGCAACTGTCCGTCGGCGTGGCGTCAAAATTTCTGA 667
RESULT 6
ID AEA03009 standard; DNA; 830 BP.
XX
AC AEA03009;
XX
XX 28-JUL-2005 (first entry)
XX DE *Neisseria meningitidis* meningococcal meningitis DNA SEQ ID NO:35.
XX
XX tumor; neoplasm; gene therapy; immunotherapy; cytostatic; meningitis;
KW gene; ds.

Db 383 TACAGCATCGCGCTCCGCGCATTTACGACTTCGACACCCCAATCCCGGTCAAAACCGTAT 442
Qy 301 CTCGGCGCGCTTTGAGCTCAACGGCGCTCCGTTCGACTTGGCGGCGAGCAGAGTTTC 360
Db 443 CTCGGCGCGCTTTGAGCTCAACGGCGCTCCGTTCGACTTGGCGGCGAGCAGAGTTTC 502
Qy 361 AGCCAAACCTCCATCGGCTCGGCGTATTGACGGGCGTAAAGCTATGCGGTTACCCCGAAT 420
Db 503 AGCCAAACCTCCATCGGCTCGGCGTATTGACGGGCGTAAAGCTATGCGGTTACCCCGAAT 562
Qy 421 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAAC 480
Db 563 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAAC 622
Qy 481 GTCGCTTCCGCGCAACTGTCGCTCGGCGTGGCGCTCAAAATTCGA 525
Db 623 GTCGCTTCCGCGCAACTGTCGCTCGGCGTGGCGCTCAAAATTCGA 667

RESULT 7
AAA81490_14/c
Continuation (15 of 15) of AAA81490 from base 1400001 (N. meningitidis B full length gen
WP Sequence split into 15 fragments LOCUS AAA81490 Accession Aaa81490
WP Fragment Name Begin End
WP AAA81490_00 1 110000
WP AAA81490_01 100001 210000
WP AAA81490_02 200001 310000
WP AAA81490_03 300001 410000
WP AAA81490_04 400001 510000
WP AAA81490_05 500001 610000
WP AAA81490_06 600001 710000
WP AAA81490_07 700001 810000
WP AAA81490_08 800001 910000
WP AAA81490_09 900001 1010000
WP AAA81490_10 1000001 1110000
WP AAA81490_11 1100001 1210000
WP AAA81490_12 1200001 1310000
WP AAA81490_13 1300001 1410000
WP AAA81490_14 1400001 1437668

Query Match 99.4%; Score 521.8; DB 3; Length 37668;
Best Local Similarity 99.6%; Pred. No. 9.4e-124;
Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAAAAAGCATTGCCACACTGATTCGCCCTCGCTCTCCGCGCGCGCACTCGCGGAA 60
Db 20578 ATGAAAAAGCATTGCCACACTGATTCGCCCTCGCTCTCCGCGCGCGCACTCGCGGAA 20519

Qy 61 GCGCATCCGCGCTTTTACGTCCAGCCGATGCCGACACGCAAAAGCTCAAGCTCTTTA 120
Db 20518 GCGCATCCGCGCTTTTACGTCCAGCCGATGCCGACACGCAAAAGCTCAAGCTCTTTA 20459

Qy 121 GGTTCGCAAAAGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACTCCGC 180
Db 20458 GGTTCGCAAAAGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACTCCGC 20399

Qy 181 TTCGCGCTCGATTCACGCGTACAAAACCTATAAGCCCATCCACCGATTTCAAACCTT 240
Db 20398 TTCGCGCTCGATTCACGCGTACAAAACCTATAAGCCCATCCACCGATTTCAAACCTT 20339

Qy 241 TACAGCATCGGCGCTCCGCGATTTACGACTTCGACACCCCAATCCCGGTCAAAACCGTAT 300
Db 20338 TACAGCATCGGCGCTCCGCGATTTACGACTTCGACACCCCAATCCCGGTCAAAACCGTAT 20279

Qy 301 CTCGGCGCGCTTTGAGCTCAACGGCGCTCCGTTCGACTTGGCGGCGAGCAGAGTTTC 360
Db 20278 CTCGGCGCGCTTTGAGCTCAACGGCGCTCCGTTCGACTTGGCGGCGAGCAGAGTTTC 20219

Qy 361 AGCCAAACCTCCATCGGCTCGGCGTATTGACGGGCGTAAAGCTATGCGGTTACCCCGAAT 420
Db 20218 AGCCAAACCTCCATCGGCTCGGCGTATTGACGGGCGTAAAGCTATGCGGTTACCCCGAAT 20159

Qy 421 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAAC 480

Db 20158 GTCGATTTGGATGCGGCTACCGCTACCACTACATCGGCAAAAGTCAACACTGTCAAAAAC 20099
Qy 481 GTCGCTTCCGCGCAACTGTCGCTCGGCGTGGCGCTCAAAATTCGA 525
Db 20098 GTCGCTTCCGCGCAACTGTCGCTCGGCGTGGCGCTCAAAATTCGA 20054

RESULT 8
AAA81490_06/c
Continuation (7 of 15) of AAA81490 from base 600001 (N. meningitidis B full length genom
WP Sequence split into 15 fragments LOCUS AAA81490 Accession Aaa81490
WP Fragment Name Begin End
WP AAA81490_00 1 110000
WP AAA81490_01 100001 210000
WP AAA81490_02 200001 310000
WP AAA81490_03 300001 410000
WP AAA81490_04 400001 510000
WP AAA81490_05 500001 610000
WP AAA81490_06 600001 710000
WP AAA81490_07 700001 810000
WP AAA81490_08 800001 910000
WP AAA81490_09 900001 1010000
WP AAA81490_10 1000001 1110000
WP AAA81490_11 1100001 1210000
WP AAA81490_12 1200001 1310000
WP AAA81490_13 1300001 1410000
WP AAA81490_14 1400001 1437668

Query Match 99.4%; Score 521.8; DB 3; Length 110000;
Best Local Similarity 99.6%; Pred. No. 1.2e-123;
Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAAAAAGCATTGCCACACTGATTCGCCCTCGCTCTCCGCGCGCGCACTCGCGGAA 60
Db 90785 ATGAAAAAGCATTGCCACACTGATTCGCCCTCGCTCTCCGCGCGCGCACTCGCGGAA 90726

Qy 61 GCGCATCCGCGCTTTTACGTCCAGCCGATGCCGACACGCAAAAGCTCAAGCTCTTTA 120
Db 90725 GCGCATCCGCGCTTTTACGTCCAGCCGATGCCGACACGCAAAAGCTCAAGCTCTTTA 90666

Qy 121 GGTTCGCAAAAGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACTCCGC 180
Db 90665 GGTTCGCAAAAGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACTCCGC 90606

Qy 181 TTCGCGCTCGATTCACGCGTACAAAACCTATAAGCCCATCCACCGATTTCAAACCTT 240
Db 90605 TTCGCGCTCGATTCACGCGTACAAAACCTATAAGCCCATCCACCGATTTCAAACCTT 90546

Qy 241 TACAGCATCGGCGCTCCGCGATTTACGACTTCGACACCCCAATCCCGGTCAAAACCGTAT 300
Db 90545 TACAGCATCGGCGCTCCGCGATTTACGACTTCGACACCCCAATCCCGGTCAAAACCGTAT 90486

Qy 301 CTCGGCGCGCTTTGAGCTCAACGGCGCTCCGTTCGACTTGGCGGCGAGCAGAGTTTC 360
Db 90485 CTCGGCGCGCTTTGAGCTCAACGGCGCTCCGTTCGACTTGGCGGCGAGCAGAGTTTC 90426

Qy 361 AGCCAAACCTCCATCGGCTCGGCGTATTGACGGGCGTAAAGCTATGCGGTTACCCCGAAT 420
Db 90425 AGCCAAACCTCCATCGGCTCGGCGTATTGACGGGCGTAAAGCTATGCGGTTACCCCGAAT 90366

Qy 421 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAAC 480
Db 90365 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAAC 90306

Qy 481 GTCGCTTCCGCGCAACTGTCGCTCGGCGTGGCGCTCAAAATTCGA 525
Db 90305 GTCGCTTCCGCGCAACTGTCGCTCGGCGTGGCGCTCAAAATTCGA 90261

RESULT 9

AAF21608/c

ID AAF21608 standard; DNA; 349980 BP.

XX AAF21608;
 AC 13-MAR-2001 (first entry)
 DT Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.
 DE Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
 KW Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
 KW diagnosis; antigen; detection; infection; gene therapy; antibacterial;
 OS ds.
 XX Neisseria meningitidis.
 XX WO200066791-A1.
 XX 09-NOV-2000.
 XX 08-MAR-2000; 2000WO-US005928.
 XX 30-APR-1999; 99US-0132068P.
 XX 08-OCT-1999; 99WO-US023573.
 XX 28-FEB-2000; 2000GB-00004695.
 XX (CHIR) CHIRON CORP.
 XX (GENO-) INST GENOMIC RES.
 XX Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC;
 XX Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
 XX Rappuoli R, Frazer CM, Grandi G;
 XX WPI; 2000-647603/62.
 XX Neisseria meningitidis B full length genome sequence and open reading
 frames are used to detect, treat and prevent Neisserial infections.
 XX Claim 7; Appendix A; 692pp; English.
 XX The present invention describes the full length genome of Neisseria
 meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
 represent fragments of the NMB genomic sequence, as the sequence was too
 long to go in a record on its own it was split into 8 sequences which
 overlap each other at the beginning and end of each sequence by 49980 bp
 (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
 AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
 AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
 given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
 primers which are used in the exemplification of the present invention.
 XX The NMB genome and fragments from it have antibacterial activity, and can
 be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
 and/or antibodies which binds to the proteins can be used in compositions
 for treating or preventing infection due to Neisserial bacteria or as a
 diagnostic reagent for detecting the presence of Neisserial bacteria or
 of antibodies raised to Neisserial bacteria. Computers, computer memory,
 computer storage medium or computer databases can be used in a search to
 identify open reading frames (ORFs) or coding sequences within the NMB
 genome. The DNA sequences provide further opportunities to find antigenic
 or immunogenic proteins which are more effective in vaccines than the
 outer membrane proteins currently used
 XX Sequence 349980 BP; 82523 A; 82940 C; 96712 G; 87805 T; 0 U; 0 Other;
 Query Match 99.4%; Score 521.8; DB 3; Length 349980;
 Best Local Similarity 99.6%; Pred. No. 1.6e-123;
 Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGAAAAAGACACTTGCACACTGATTCCTCGCTCTCCGCGCGCGCACTGCGGAA 60
 Db 90786 ATGAAAAAGACACTTGCACACTGATTCCTCGCTCTCCGCGCGCGCACTGCGGAA 90727
 QY 61 GCGCGATCCGCTTTTACGTCCAGCCGATGCGCGACACGCAAAAGCTCTCAAGCTCTTTA 120
 Db 90726 GCGCGATCCGCTTTTACGTCCAGCCGATGCGCGACACGCAAAAGCTCTCAAGCTCTTTA 90667

QY 121 GGTTCTGCCAAGGCTTCAGCCCG
 Db 90666 GGTTCTGCCAAGGCTTCAGCCCG
 QY 181 TTGCGCGTGCATTACAGCGCTACAAA
 Db 90606 TTGCGCGTGCATTACAGCGCTACAAA
 QY 241 TACAGCATCGCGCTCGCCATTACCG
 Db 90546 TACAGCATCGCGCTCGCCATTACCG
 QY 301 CTGCGCGCGCTTGAGCCTCAACGGCGCC
 Db 90486 CTGCGCGCGCTTGAGCCTCAACGGCGCC
 QY 361 AGCCAAACCTCCATCGCGCTCGCGGTATTGAC
 Db 90426 AGCCAAACCTCCATCGCGCTCGCGGTATTGAC
 QY 421 GTCGATTTGGATCGCGCTACCGCTACAACTTACI
 Db 90366 GTCGATTTGGATCGCGCTACCGCTACAACTTACI
 QY 481 GTCGCTTCGCGCGAACTGTCGCGCTCGCGCTCAAAATTCGA 525
 Db 90306 GTCGCTTCGCGCGAACTGTCGCGCTCGCGCTCAAAATTCGA 90262
 RESULT 10
 AAT39041
 ID AAT39041 standard; DNA; 850 BP.
 AC AAT39041;
 XX 16-OCT-2003 (revised)
 DT 22-DEC-1996 (first entry)
 DE Proteinase K resistant N. meningitidis 22 kD surface protein
 KW Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae,
 KW antibody; detection; probe; surface protein; ss.
 XX Neisseria meningitidis; strain Z4063.
 PH Key Location/Qualifiers
 FT CDS 208..732
 FT sig_peptide 208..264 /*tag= a
 FT mat_peptide 265..729 /*tag= b
 FT mat_peptide 265..729 /*tag= c
 XX WO9629412-A1.
 PN 26-SEP-1996.
 XX 15-MAR-1996; 96WO-CA000157.
 XX 17-MAR-1995; 95US-00406362.
 PR 04-AUG-1995; 95US-0001983P.
 XX (IAPB-) IAP BIO VAC INC.
 XX Brodeur BR, Martin D, Hamel J, Rioux C;
 XX WPI; 1996-443187/44.
 DR P-PSDB; AAW04893.
 XX Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against, or
 PT diagnosis of, N. meningitidis infection.
 XX

PS Claim 12; Fig 9; 117pp; English.

XX A proteinase K resistant surface protein has been isolated from 4 strains

CC of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,

CC antigenic fragments of antibodies can be used in a vaccine for the

CC prevention of infection by N. meningitidis or by N. gonorrhoeae in

CC humans. The antibodies may also be used diagnostically to detect N.

CC meningitidis infection. The antigen may also be used to detect antibodies

CC specific to N. meningitidis antigen. DNA sequences encoding the antigen,

CC or their fragments, can be used as probes for the detection of pathogenic

CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)

XX

SQ Sequence 850 BP; 208 A; 273 C; 185 G; 184 T; 0 U; 0 Other;

Query Match 98.8%; Score 518.6; DB 2; Length 850;

Best Local Similarity 99.2%; Pred. No. 2.6e-123; Indels 0; Gaps 0;

Matches 521; Conservative 0; Mismatches 4;

Qy 1 ATGAAAAAGCATTGGCCACACTGATTGCCCTCTCTCCGGCGCGGCACTGGCGGAA 60

Db 208 ATGAAAAAGCATTGGCCACACTGATTGCCCTCTCTCCGGCGCGGCACTGGCGGAA 267

Qy 61 GGCGCATCGGCTTTTACGTCGAAGCGATGCCGACACGCAAAAGCTCAAGCTCTTTA 120

Db 268 GGCGCATCGGCTTTTACGTCGAAGCGATGCCGACACGCAAAAGCTCAAGCTCTTTA 327

Qy 121 GGTTCGTCGAAGGCTTCAGCGCGCATCTCCGAGGCTACCGCATCAAGGACTCCGC 180

Db 328 GGTTCGTCGAAGGCTTCAGCGCGCATCTCCGAGGCTACCGCATCAAGGACTCCGC 387

Qy 181 TTGCGCGTCGATTACAGCGCTACAAAACTATATAAGCCCATCCACCGATTTCAAACTT 240

Db 388 TTGCGCGTCGATTACAGCGCTACAAAACTATATAAGCCCATCCACCGATTTCAAACTT 447

Qy 241 TACAGCATCGGCGCTCGGCATTACGATTCGACACCCCAATCGCCGTCGCAACCGTAT 300

Db 448 TACAGCATCGGCGCTCGGCATTACGATTCGACACCCCAATCGCCGTCGCAACCGTAT 507

Qy 301 CTGCGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTGGCGGCGAGGAGCTTC 360

Db 508 CTGCGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTGGCGGCGAGGAGCTTC 567

Qy 361 AGCCAAACCTCCACCGCTCGGCTATTTGACGGGCGTAAAGCTATGCGGTTACCCCGAAT 420

Db 568 AGCCAAACCTCCACCGCTCGGCTATTTGACGGGCGTAAAGCTATGCGGTTACCCCGAAT 627

Qy 421 GTCGATTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480

Db 628 GTCGATTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 687

Qy 481 GTCCGTTCCGCGAAGTGTCCGTCGGGCTGCGGCTCAAAATCTCGA 525

Db 688 GTCCGTTCCGCGAAGTGTCCGTCGGGCTGCGGCTCAAAATCTCGA 732

RESULT 11

AB567381

ID AB567381 standard; DNA; 710 BP.

XX

AC AB567381;

XX

DT 29-NOV-2002 (first entry)

XX

DE Neisseria gonorrhoeae outer membrane gene #1.

XX

KW Gram-negative bacterial bleb; PorB; outer membrane protein;

KW Chlamydia trachomatis infection; Chlamydia pneumoniae infection;

KW protective antigen; antibacterial; vaccine; gene; ds.

XX

OS Neisseria gonorrhoeae.

XX

FN WO200262380-A2

XX

PD 15-AUG-2002.

XX

PP 08-FEB-2002; 2002WO-EP001356.

XX

PR 08-FEB-2001; 2001GB-00003169.

XX

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX

PI Berthet FJ, Lobet Y, Poolman J, Verlant VGCL;

XX

DR WPI; 2002-657510/70.

DR P-PSDB; ABG91063.

XX

PT Novel gram-negative bacterial bleb presenting on its surface PorB outer

PT membrane protein from Chlamydia trachomatis or protective antigen from

PT Chlamydia pneumoniae, useful for preventing Chlamydia infection.

XX

PS Disclosure; Page 54; 75pp; English.

XX

CC The present invention relates to a new gram-negative bacterial bleb

CC presenting on its surface the PorB outer membrane protein from Chlamydia

CC trachomatis, or a protective antigen from C. pneumoniae. The invention is

CC useful for preventing C. trachomatis or C. pneumoniae infection in a

CC host. The present nucleic acid sequence represents a Neisseria

CC gonorrhoeae gene as described in the invention

XX

SQ Sequence 710 BP; 171 A; 228 C; 160 G; 151 T; 0 U; 0 Other;

Query Match 95.7%; Score 502.6; DB 6; Length 710;

Best Local Similarity 97.3%; Pred. No. 3.2e-119;

Matches 511; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGAAAAAGCATTGGCCACACTGATTGCCCTCTCCGGCGCGGCACTGGCGGAA 60

Db 141 ATGAAAAAGCATTGGCCACACTGATTGCCCTCTCCGGCGCGGCACTGGCGGAA 200

Qy 61 GGCGCATCGGCTTTTACGTCGAAGCGGATGCCGACACGCAAAAGCTCAAGCTCTTTA 120

Db 201 GGCGCATCGGCTTTTACGTCGAAGCGGATGCCGACACGCAAAAGCTCAAGCTCTTTA 260

Qy 121 GGTTCGTCGAAGGCTTCAGCGCGCATCTCCGAGGCTACCGCATCAAGGACTCCGC 180

Db 261 GGTTCGTCGAAGGCTTCAGCGCGCATCTCCGAGGCTACCGCATCAAGGACTCCGC 320

Qy 181 TTGCGCGTCGATTACAGCGCTACAAAACTATATAAGCCCATCCACCGATTTCAAACTT 240

Db 321 TTGCGCGTCGATTACAGCGCTACAAAACTATATAAGCCCATCCACCGATTTCAAACTT 380

Qy 241 TACAGCATCGGCGCTCGGCATTACGATTCGACACCCCAATCGCCGTCGCAACCGTAT 300

Db 381 TACAGCATCGGCGCTCGGCATTACGATTCGACACCCCAATCGCCGTCGCAACCGTAT 440

Qy 301 CTGCGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTGGCGGCGAGGAGCTTC 360

Db 441 CTGCGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTGGCGGCGAGGAGCTTC 500

Qy 361 AGCCAAACCTCCATCGGCTCGGCTATTTGACGGGCGTAAAGCTATGCGGTTACCCCGAAT 420

Db 501 AGCCAAACCTCCGCGGCGCTCGGCTATTTGCGGCGGCTAAAGCTATGCGGTTACCCCGAAT 567

Qy 421 GTCGATTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 525

Db 561 GTCGATTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 621

Qy 481 GTCCGTTCCGCGAAGTGTCCGTCGGGCTGCGGCTCAAAATCTCGA 525

Db 621 GTCCGTTCCGCGAAGTGTCCGTCGGGCTGCGGCTCAAAATCTCGA 567

RESULT 12

AAT39042

ID AAT39042 standard; DNA; 810 BP

XX

4
Lhp

CC meningitis infection. The antigen may also be used to detect antibodies
CC specific to N. meningitidis antigen. DNA sequences encoding the antigen,
CC or their fragments, can be used as probes for the detection of pathogenic
CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 710 BP; 174 A; 232 C; 148 G; 156 T; 0 U; 0 Other;

Query Match 93.6%; Score 491.2; DB 2; Length 710;
Best Local Similarity 97.0%; Pred. No. 2.8e-116;
Matches 512; Conservative 0; Mismatches 13; Indels 3; Gaps 1;

Qy 1 ATGAAAAGACCTTGCCACACTGATGCCCTCTCTCCGGCGCGCACTGCGGAA 60
Db 116 ATGAAAAGACCTTGCGCACTGATGCCCTCTCCGGCGCGCACTGCGGAA 175
Qy 61 GGCGCATCCGGCTTTAGCTCAAGCCGATGCCGACACGAAAGCTCAAGCTCTTTA 120
Db 176 GGCGCATCCGGCTTTAGCTCAAGCCGATGCCGACACGAAAGCTCAAGCTCTTTA 235
Qy 121 GGTTCGCAAGGCTTCAGCCCGCATCTCCGAGGCTACCGCATCAAGCACTCCGC 180
Db 236 GGTTCGCAAGGCTTCAGCCCGCATCTCCGAGGCTACCGCATCAAGCACTCCGC 295
Qy 181 TTCCCGCTCGATTACAGCGCTACAAAAAATATA---AAGCCCATCCACCGATTTCAA 237
Db 296 TTCCCGCTCGATTACAGCGCTACAAAAAATATA---AAGCCCATCCACCGATTTCAA 355
Qy 238 CTTTACAGCATCGGGGCTCGGCATTTAGCACTTCGACCTTCGACCCGATCCCGTCAACCG 297
Db 356 CTTTACAGCATCGGGGCTCGGCATTTAGCACTTCGACCTTCGACCCGATCCCGTCAACCG 415
Qy 298 TATCTCGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTTGGGCGGCGAGCAGC 357
Db 416 TATCTCGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTTGGGCGGCGAGCAGC 475
Qy 358 TTACGCAAACTCCATCGGCTCGGGCTATTGACGGCGTAAAGCTATGCCGTTACCCCG 417
Db 476 TTACGCAAACTCCACCGGCTCGGGCTATTGCGGGCGTAAAGCTATGCCGTTACCCCG 535
Qy 418 AATGTCGATTTGGATCGCGCTAGCGCTAGCACTACATACGCAAGTCAACACTGTCAA 477
Db 536 AATGTCGATTTGGATCGCGCTAGCGCTAGCACTACATACGCAAGTCAACACTGTCAA 595
Qy 478 AACGTCGCTTCGGGAACTGTCCGTCGGCGTGGCGCTCAAAATTCGA 525
Db 596 AATGTCGCTTCGGGAACTGTCCGTCGGCGTGGCGCTCAAAATTCGA 643

RESULT 14
ABZ38961
ID ABZ38961 standard; DNA; 525 BP.

XX AC ABZ38961;

XX DT 07-MAR-2003 (first entry)

XX DE N. gonorrhoeae nucleotide sequence SEQ ID 2511.

XX KW Antibacterial; infection; vaccine; gene therapy; gene; ds.

XX OS Neisseria gonorrhoeae.

XX PN W0200279243-A2.

XX FD 10-OCT-2002.

XX PF 12-FEB-2002; 2002WO-IB002069.

XX PR 12-FEB-2001; 2001GB-00003424.

XX PA (CHIR-) CHIRON SPA.

XX PI Fontana MR, Pizza M, Masignani V, Monaci E;

XX WPI; 2003-058415/05.
DR P-PSDB; ABP77991.

XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a
PT medicament for treating or preventing N. gonorrhoeae infection.

XX PS Disclosure; Page 371; 815pp; English.

XX The present invention relates to proteins from Neisseria gonorrhoeae.
CC Also disclosed are the nucleic acid molecules encoding the proteins and
CC antibodies that specifically bind to the proteins. The composition
CC comprising the protein, nucleic acid or antibody is useful for the
CC manufacture of a medicament for treating or preventing N. gonorrhoeae
CC infection, this may be in the form of a vaccine or gene therapy.

CC Sequences given in records ABZ37706-ABZ42016 represent nucleic acid
CC molecules of the invention

XX SQ Sequence 525 BP; 117 A; 188 C; 120 G; 100 T; 0 U; 0 Other;

Query Match 91.5%; Score 480.2; DB 10; Length 525;
Best Local Similarity 96.0%; Pred. No. 1.7e-113;
Matches 504; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

Qy 1 ATGAAAAGACCTTGCCACACTGATGCCCTCTCCGGCGCGCACTGCGGAA 60
Db 1 ATGAAAAGACCTTGCGCACTGATGCCCTCTCCGGCGCGCACTGCGGAA 60
Qy 61 GGCGCATCCGGCTTTAGCTCAAGCCGATGCCGACACGAAAGCTCAAGCTCTTTA 120
Db 61 GGCGCATCCGGCTTTAGCTCAAGCCGATGCCGACACGAAAGCTCAAGCTCTTTA 120
Qy 121 GGTTCGCAAGGCTTCAGCGCGCATCTCCGAGGCTACCGCATCAAGCACTCCGC 180
Db 121 GGTTCGCAAGGCTTCAGCGCGCATCTCCGAGGCTACCGCATCAAGCACTCCGC 180
Qy 181 TTCCCGCTCGATTACAGCGCTACAAAAAATATA---AAGCCCATCCACCGATTTCAA 237
Db 181 TTCCCGCTCGATTACAGCGCTACAAAAAATATA---AAGCCCATCCACCGATTTCAA 240
Qy 238 CTTTACAGCATCGGGGCTCGGCATTTAGCACTTCGACACCCGATCCCGTCAACCG 297
Db 241 CTTTACAGCATCGGGGCTCGGCATTTAGCACTTCGACACCCGATCCCGTCAACCG 300
Qy 298 TATCTCGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTTGGGCGGCGAGCAGC 357
Db 301 TATCTCGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTTGGGCGGCGAGCAGC 360
Qy 358 TTACGCAAACTCCATCGGCTCGGGCTATTGACGGCGGTAAGCTATGCCGTTACCCCG 417
Db 361 TTACGCAAACTCCGCGCGCTCGGGCTATTGCGGGCGTAAAGCTATGCCGTTACACCC 420
Qy 418 AATGTCGATTTGGATCGGGCTACCGCTACACTACATCGGCAAGTCAACACTGTCAA 477
Db 421 AATGTCGATTTGGATCGGGCTACCGCTACACTACATCGGCAAGTCAACACTGTCAA 480
Qy 478 AACGTCGCTTCGGGAACTGTCCGTCGGCGTGGCGCTCAAAATTC 522
Db 481 AACGTCGCTTCGGGAACTGTCCGTCGGCGTGGCGCTCAAAATTC 525

RESULT 15

ADL13425

ID ADL13425 standard; DNA; 468 BP.

XX AC ADL13425;

XX DT 03-JUN-2004 (first entry)

XX DE Neisseria meningitidis H44/76 mature NspA-encoding DNA.

XX KW Neisserial surface protein A; NspA; refolding; recombinant production;
KW vaccine; subunit vaccine; prevention; diagnosis; meningococcus;

KW invasive bacterial disease; bacteraemia; meningitis;
 KW Neisseria gonorrhoeae; gonorrhoea; mature protein; strain H44/76;
 KW antibacterial; gene therapy; gene; ds.
 OS Neisseria meningitidis; H44/76.

Key Location/Qualifiers
 CDS 1..468
 FT /tag= b
 FT /partial
 FT /product= "Mature NspA"
 FT /note= "No start codon given"
 FT mat_peptide 1..465
 FT /tag= a
 FT /product= "Mature NspA"

WO2004020452-A2.

PD 11-MAR-2004.

XX 28-AUG-2003; 2003WO-EP010085.

XX 30-AUG-2002; 2002GB-00020197.

XX (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
 XX (UYUT-) RIJKSUNIV UTRECHT.

XX Biemans R, Bos M, Denoel P, Feron C, Goraj K, Poolman J;
 XX Tommassen J, Weynants V;

XX WPI; 2004-239150/22.

DR P-ESDB; ADL13426.

XX New refolded NspA protein, useful for preparing a composition for
 PT diagnosing, treating or preventing infection caused by Neisseria
 PT meningitidis or Neisseria gonorrhoeae.

XX Example 1; Fig 2; 62pp; English.

XX The invention relates to an isolated refolded Neisserial surface protein
 CC A (NspA) from Neisseria meningitidis or Neisseria gonorrhoeae. The
 CC invention also relates to the method of refolding an NspA protein; an
 CC alkaline refolding buffer comprising ethanolamine and SB-12 (3-
 CC dimethyldeacylammonioethanesulphonate) for refolding an NspA protein; a
 CC pharmaceutical composition comprising the refolded NspA protein, a
 CC carrier and optionally one or more other Neisserial antigens; a method of
 CC preventing or treating a Neisserial infection; an antibody immunospecific
 CC for the NspA protein; and diagnosing a Neisserial infection. NspA has
 CC characteristics which indicate that it is a potential vaccine candidate
 CC for the development of subunit vaccines for the treatment of infections
 CC caused by Neisseria meningitidis (meningococcus), which causes invasive
 CC bacterial diseases such as bacteraemia and meningitis, or Neisseria
 CC gonorrhoeae, the causative agent of gonorrhoea. Recombinantly produced
 CC NspA could therefore be used to produce vaccine compositions and it could
 CC also be used in the development of new antimicrobial agents, diagnostic
 CC tests and in drug screening. However, recombinantly produced proteins are
 CC frequently unable to adopt their biologically active conformations, and
 CC yields may be very low due to mis-folding and aggregation of the protein.
 CC The method of the invention provides an improved method for refolding the
 CC NspA protein, and it is possible to increase the recovery of active
 CC protein form partly purified inclusion bodies in amounts up to 100%
 CC without the need for further purification. The refolded NspA protein is
 CC useful for preparing a composition for diagnosing, treating or preventing
 CC infection caused by Neisseria meningitidis or Neisseria gonorrhoeae. The
 CC present sequence represents DNA encoding the mature NspA protein from
 CC Neisseria meningitidis H44/76 which was amplified and cloned in an
 CC example of the invention.

SQ Sequence 468 BP; 105 A; 164 C; 106 G; 93 T; 0 U; 0 Other;

Query Match 88.5%; Score 464.8; DB 12; Length 468;
 Best Local Similarity 99.6%; Pred. NO. 1.5e-109;
 Matches 466; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCGCATCCGCTTTTACGTCAAGCCGATGCGGCACACGCAAAAGCCTCAAGCTCT 117
 DB 1 GAAGCGCATCCGCTTTTACGTCAAGCCGATGCGGCACACGCAAAAGCCTCAAGCTCT 60
 QY 118 TTAGGTTCTGCCAAAGGCTTCAGCCCGGCTCTCCGAGGCTACCGCATCAACGACCTC 177
 DB 61 TTAGGTTCTGCCAAAGGCTTCAGCCCGGCTCTCCGAGGCTACCGCATCAACGACCTC 120
 QY 178 CGCTTCGCGCTCGATTACACGCGCTACAAAACCTATAAAGCCCCCATCCACCGATTTCAAA 237
 DB 121 CGCTTCGCGCTCGATTACACGCGCTACAAAACCTATAAAGCCCCCATCCACCGATTTCAAA 180
 QY 238 CTTTACAGCATCGCGCGCTCCGCCATTTCACGCTTCGACACCCCAATCCCGTCAAAACG 297
 DB 181 CTTTACAGCATCGCGCGCTCCGCCATTTCACGCTTCGACACCCCAATCCCGTCAAAACG 240
 QY 298 TATCTCGCGCGCGCTTCAGGCTCAACGCGGCTCCGTCGACTTGGGCGGCGAGCAGC 357
 DB 241 TATCTCGCGCGCGCTTCAGGCTCAACGCGGCTCCGTCGACTTGGGCGGCGAGCAGC 300
 QY 358 TTCAGCCAAACCTCCATCGGCTCGGCGTATTGACGGGCGTAAGCTATGCGGTTACCCCG 417
 DB 301 TTCAGCCAAACCTCCATCGGCTCGGCGTATTGACGGGCGTAAGCTATGCGGTTACCCCG 360
 QY 418 AATGTCGATTGGATGCGGCTACCGCTACAACCTACATCGGCAAGTCAACACTGTCAAA 477
 DB 361 AATGTCGATTGGATGCGGCTACCGCTACAACCTACATCGGCAAGTCAACACTGTCAAA 420
 QY 478 AACGTCGTTCCGGGGAACCTGTCGTCGGGCGGCGGCTCAAAATTCGA 525
 DB 421 AACGTCGTTCCGGGGAACCTGTCGTCGGGCGGCGGCTCAAAATTCGA 468

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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Listing first 45 summaries

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- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	525	100.0	830	3	US-08-913-362-1
2	518.6	98.8	850	3	US-08-913-362-5
3	502.6	95.7	810	3	US-08-913-362-7
4	501.2	95.5	528	3	US-08-913-362-29
5	491.2	93.6	710	3	US-08-913-362-3
6	49.8	9.5	1919	3	US-09-614-912-175
7	45.6	8.7	4403765	3	US-09-103-840A-2
8	45.6	8.7	4411529	3	US-09-103-840A-1
9	45	8.6	4403765	3	US-09-103-840A-2
10	45	8.6	4411529	3	US-09-103-840A-1
11	44	8.4	1082	3	US-09-881-165-4
12	44	8.4	4483	3	US-08-961-527-363
13	44	8.4	32768	3	US-08-961-527-71
14	43.6	8.3	390	3	US-09-197-649-7
15	43	8.2	925	3	US-08-858-003-1
16	43	8.2	925	3	US-09-078-166-1
17	43	8.2	925	3	US-08-997-467-1
18	42.8	8.2	2434	3	US-09-902-540-3527
19	42.8	8.2	18538	3	US-09-902-540-1169
20	42.4	8.1	36519	3	US-08-923-137-2
21	42	8.0	620	3	US-08-961-527-374
22	42	8.0	1859	3	US-08-894-818B-15
23	42	8.0	1859	3	US-08-841-553-15
24	42	8.0	1977	3	US-08-894-818B-2

25	42	8.0	1977	3	US-08-894-818B-6	Sequence 6, Appli
26	42	8.0	1977	3	US-09-445-472-11	Sequence 11, Appli
27	42	8.0	1977	3	US-10-090-624-11	Sequence 11, Appli
28	42	8.0	1977	3	US-09-841-553-2	Sequence 2, Appli
29	42	8.0	1977	3	US-09-841-553-6	Sequence 6, Appli
30	41.6	7.9	867	3	US-09-216-333B-340	Sequence 340, App
31	41.6	7.9	867	3	US-09-216-333B-342	Sequence 342, App
32	41.6	7.9	1397	3	US-09-216-333B-343	Sequence 343, App
33	41.6	7.9	1397	3	US-09-216-333B-345	Sequence 345, App
C 34	41.4	7.9	1614	3	US-09-489-039A-3484	Sequence 3484, Ap
C 35	41.4	7.9	1698	3	US-09-489-039A-3505	Sequence 3505, Ap
36	41.4	7.9	1706	3	US-10-033-109-3	Sequence 3, Appli
37	41.4	7.9	3486	3	US-09-614-221A-292	Sequence 292, App
38	41.4	7.9	25254	3	US-09-902-540-1233	Sequence 1233, Ap
39	41.4	7.9	58857	3	US-09-477-962-1	Sequence 1, Appli
40	41.2	7.8	1781	3	US-09-675-018B-7	Sequence 7, Appli
41	41.2	7.8	1781	3	US-10-428-041-7	Sequence 7, Appli
42	41.2	7.8	1889	3	US-09-675-018B-9	Sequence 9, Appli
43	41.2	7.8	1889	3	US-10-428-041-9	Sequence 9, Appli
C 44	41	7.8	1439	3	US-09-056-556-167	Sequence 167, App
C 45	41	7.8	1439	3	US-09-072-596-162	Sequence 162, App

ALIGNMENTS

RESULT 1
US-08-913-362-1
; Sequence 1, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josée
; APPLICANT: Rioux, Clément
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913.362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406.362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001.983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 830 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

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; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: 608B
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 143..667
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 143..199
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 200..667
US-08-913-362-1

Query Match 100.0%; Score 525; DB 3; Length 830;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAAGACCTTGCCACACTGATGCGCTCTCCGCGCGCGCGCACTGGCGGAA 60
DB 143 ATGAAAAGACCTTGCCACACTGATGCGCTCTCCGCGCGCGCGCACTGGCGGAA 202
QY 61 GCGCATCCGGCTTTTACGTCACAGCGATGCGGCACACGCAAAAGCCTCAAGCTCTTTA 120
DB 203 GGCGCATCCGGCTTTTACGTCACAGCGATGCGGCACACGCAAAAGCCTCAAGCTCTTTA 262
QY 121 GGTTCGCAAAAGGTTTCCGCGCGGATCTCCGAGGCTACCGCATCAACGACTCCGC 180
DB 263 GGTTCGCAAAAGGTTTCCGCGCGGATCTCCGAGGCTACCGCATCAACGACTCCGC 322
QY 181 TTCCGGTTCGATACACGCGCTACAAAACCTATTAAGCCCATCCACGATTTCAAACTT 240
DB 323 TTCCGGTTCGATACACGCGCTACAAAACCTATTAAGCCCATCCACGATTTCAAACTT 382
QY 241 TACAGCATCCGGCGCTCGCGCATTTACGACTTCGACACCCCAATCGCCGTCAAAACCGTAT 300
DB 383 TACAGCATCCGGCGCTCGCGCATTTACGACTTCGACACCCCAATCGCCGTCAAAACCGTAT 442
QY 301 CTGCGCGCGCTTGAGCTCTCAACGCGCCCTCCGTCGACTTTGGGCGGAGGACAGCTTC 360
DB 443 CTGCGCGCGCTTGAGCTCTCAACGCGCCCTCCGTCGACTTTGGGCGGAGGACAGCTTC 502
QY 361 AGCCAAACCTCCATCGGCTCGGCTATTTACGCGGCGTAAGCTATGCCGTTACCCCGAAT 420
DB 503 AGCCAAACCTCCATCGGCTCGGCTATTTACGCGGCGTAAGCTATGCCGTTACCCCGAAT 562
QY 421 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAAC 480
DB 563 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAAC 622
QY 481 GTCGCTTCCGCGCAACTGCTCCGTCGGCGTGGCGGTCGCGTCAAAATCTGA 525
DB 623 GTCGCTTCCGCGCAACTGCTCCGTCGGCGTGGCGGTCGCGTCAAAATCTGA 667

RESULT 2
US-08-913-362-5
; Sequence 5, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; NUMBER OF INVENTIONS: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
```

```
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/POCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 850 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: Z4063
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 208..732
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 208..264
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 265..732
US-08-913-362-5

Query Match 98.8%; Score 518.6; DB 3; Length 850;
Best Local Similarity 99.2%; Pred. No. 6.8e-130;
Matches 521; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGAAAAGACCTTGCCACACTGATGCGCTCTCCGCGCGCGCGCACTGGCGGAA 60
DB 208 ATGAAAAGACCTTGCCACACTGATGCGCTCTCCGCGCGCGCGCACTGGCGGAA 267
QY 61 GGCGCATCCGGCTTTTACGTCACAGCGATGCGGCACACGCAAAAGCCTCAAGCTCTTTA 120
DB 268 GGCGCATCCGGCTTTTACGTCACAGCGATGCGGCACACGCAAAAGCCTCAAGCTCTTTA 327
QY 121 GGTTCGCAAAAGGTTTCCGCGCGGATCTCCGAGGCTACCGCATCAACGACTCCGC 180
DB 328 GGTTCGCAAAAGGTTTCCGCGCGGATCTCCGAGGCTACCGCATCAACGACTCCGC 387
QY 181 TTCCGGTTCGATACACGCGCTACAAAACCTATTAAGCCCATCCACGATTTCAAACTT 240
DB 388 TTCCGGTTCGATACACGCGCTACAAAACCTATTAAGCCCATCCACGATTTCAAACTT 447
QY 241 TACAGCATCCGGCGCTCGCGCATTTACGACTTCGACACCCCAATCGCCGTCAAAACCGTAT 300
DB 448 TACAGCATCCGGCGCTCGCGCATTTACGACTTCGACACCCCAATCGCCGTCAAAACCGTAT 507
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QY 301 CTCGGCGCGCTTGAAGCTCAACCGCGCTCCGTCGACTTGGGCGGCGAGCAGCTTC 360
Db 508 CTCGGCGCGCTTGAAGCTCAACCGCGCTCCGTCGACTTGGGCGGCGAGCAGCTTC 567
QY 361 AGCAAACTCCATCGGCTGGCGCTATTGAGGGCGTAAGCTATGCCGTTACCCCGAAT 420
Db 568 AGCAAACTCCATCGGCTGGCGCTATTGAGGGCGTAAGCTATGCCGTTACCCCGAAT 627
QY 421 GTCGATTGGATGCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 480
Db 628 GTCGATTGGATGCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 687
QY 481 GTCGCTCCGGCGAACTGTCGCTCGCGGTGGCGGTCAAAATCTGA 525
Db 688 GTCGCTCCGGCGAACTGTCGCTCGCGGTGGCGGTCAAAATCTGA 732

RESULT 3

US-08-913-362-7
; Sequence 7, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 13-NOV-1997
; PRIORITY APPLICATION NUMBER: US/08/913.362
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 04/998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 810 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Neisseria gonorrhoeae
; STRAIN: b2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 241..765

; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 241..297
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 298..765
US-08-913-362-7
Query Match 95.7%; Score 502.6; DB 3; Length 810;
Best Local Similarity 97.3%; Pred. No. 1.3e-125;
Matches 511; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 ATGAAAAAGACATTGCCACACTGATTGCCCTCTCCCGCGCGCGCGCGGAA 60
Db 241 ATGAAAAAGACATTGCCGCACTGATTGCCCTCCGCACTCCGCGCGCGCGGAA 300
QY 61 GGCGCATCCGGCTTTTACGTCAAGCGGATCCGACACGAAAGCTTCAAGCTCTTTA 120
Db 301 GGCGCATCCGGCTTTTACGTCAAGCGGATCCGACACGCGGCTTCAAGCTCTTTA 360
QY 121 GGTTCGCAAAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACTTCGCG 180
Db 361 GGTTCGCAAAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACTTCGCG 420
QY 181 TTGCGGCTCGATTACACGCGCTACAAAACCTATAAAGCGCCATCCACCGATTCAACTT 240
Db 421 TTGCGGCTCGATTACACGCGCTACAAAACCTATAAAGCGCCATCCACCGATTCAACTT 480
QY 241 TACAGCATCGCGCGCTTCGCCATTTCAGACTTCGACACCCCAATCCCGTCAACCGTAT 300
Db 481 TACAGCATCGCGCGCTTCGCCATTTCAGACTTCGACACCCCAATCCCGTCAACCGTAT 540
QY 301 CTCGGCGCGCTTTGAGCTCAACCGCGCTCCGTCGACTTGGGCGGCGAGCAGCTTC 360
Db 541 TTCGGCGCGCTTTGAGCTCAACCGCGCTCCGCGCTTGGGCGGCGAGCAGCTTC 600
QY 361 AGCAAACTCCATCGCGCTCGGCTGATTGAGCGGCTTAAGCGGCTTAAGCTATCCCGGAT 420
Db 601 AGCAAACTCCATCGCGCTCGGCTGATTGAGCGGCTTAAGCGGCTTAAGCTATCCCGGAT 660
QY 421 GTCGATTGGATGCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 480
Db 661 GTCGATTGGATGCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 720
QY 481 GTCGCTCCGGCGAACTGTCGCTCGCGGTGGCGGTCAAAATCTGA 525
Db 721 GTCGCTCCGGCGAACTGTCGCTCGCGGTGGCGGTCAAAATCTGA 765

RESULT 4

US-08-913-362-29
; Sequence 29, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913.362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406.362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001.983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 528 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "consensus"
US-08-913-362-29

Query Match 95.5%; Score 501.2; DB 3; Length 528;
Best Local Similarity 95.1%; Pred. No. 2.8e-125;
Matches 502; Conservative 22; Mismatches 1; Indels 3; Gaps 1;

QY 1 ATGAAAAAGACACTTGCACACTGATTCGCCCTCGCTCTCCGGCGCGCGCACTGCGCGAA 60
DB 1 ATGAAAAAGACACTTGCRCACACTGATTCGCCCTCGCHCTCCCGCGCGCGCACTGCGGAA 60
QY 61 GCGGCATCCGGCTTTTAGTCTCAAGCCGATGCGGCACACGCAAAAGCTCAAGCTCTTTA 120
DB 61 GCGGCATCCGGCTTTTAGTCTCAAGCCGATGCGGCACACGCAAAAGCTCAAGCTCTTTA 120
QY 121 GGTTCGCAAGGCTTCAGCCCGCGCATCTCCGAGGCTTCGCGATCAACGACCTCCGC 180
DB 121 GGTTCGCAAGGCTTCAGCCCGCGCATCTCCGAGGCTTCGCGATCAACGACCTCCGC 180
QY 181 TTCGCGTCTGATACACGCGCTACAAAATATA---AAGCCCATCCACCGATTTCAA 237
DB 181 TTCGCGTCTGATACACGCGCTACAAAATATAAAGAGYCCCATCCACCGATTTCAA 240
QY 238 CTTTACAGCATCGCGCGTTCGCCATTTACGACTTCGACACCCAAATGCCCGTCAACCG 297
DB 241 CTTTACAGCATCGCGCGTTCGGYCATTTACGACTTCGACACCCAAATGCCCGTCAACCG 300
QY 298 TATCTCGCGCGCTTGAGCTCAACGCGCTCCGCTCGACTTGGCGCGCGACGACG 357
DB 301 TATTCGCGCGCGCTTGAGCTCAACGCGCTCCGCTCGACTTGGCGCGCGACGACG 360
QY 358 TTACGCAAACTCCATCGCGCTCGGCTATTGACGGCGGTAAGCTATGCGCTTACCCCG 417
DB 361 TTACGMAAACTCCRYCGGCTCGGCTATTGCGGCGTAAGCTATGCGCTTACCCCG 420
QY 418 AATGTCGATTTGGATGCGCGTACCGCTAACATACATCGGCAAGTCAACACTGTCAA 477
DB 421 AATGTCGATTTGGATGCGCGTACCGCTAACATACATCGGCTAAGTCAACACTGTCAA 480
QY 478 AACGTCGCTTCGCGGCACTCTCGCTCGGCTGCGCGTCAAAATCTGA 525
DB 481 AAYGTCCGTTCCGCGCAACTGTCCGTCGCGYGTTCGCGTCAAAATCTGA 528

RESULT 5
US-08-913-362-3
; Sequence 3, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
;
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913.362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001.983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 710 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: MCH88
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 116..643
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 116..172
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 173..643
; US-08-913-362-3

Query Match 93.6%; Score 491.2; DB 3; Length 710;
Best Local Similarity 97.0%; Pred. No. 1.5e-122;
Matches 512; Conservative 0; Mismatches 13; Indels 3; Gaps 1;

QY 1 ATGAAAAAGACACTTGCACACTGATTCGCCCTCGCTCTCCGGCGCGCGCACTGCGCGAA 60
DB 116 ATGAAAAAGACACTTGCRCACACTGATTCGCCCTCGCHCTCCCGCGCGCGCACTGCGGAA 175
QY 61 GCGGCATCCGGCTTTTAGTCTCAAGCCGATGCGGCACACGCAAAAGCTCAAGCTCTTTA 120
DB 176 GCGGCATCCGGCTTTTAGTCTCAAGCCGATGCGGCACACGCAAAAGCTCAAGCTCTTTA 235
QY 121 GGTTCGCAAGGCTTCAGCCCGCGCATCTCCGAGGCTTCGCGATCAACGACCTCCGC 180
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Db 236 GGTTCGTCACAAAGGCTTCAGCCGCGCATCTCGCAGGCTACCGCATCAAGCACTCCGC 295
QY 181 TTGCGCGTCGATTACACGCGCTCAAAAACCTATA---AAGCCCATTCACCGATTTCAAA 237
Db 296 TTGCGCGTCGATTACACGCGCTCAAAAACCTATAAACAAGTCCCATCCACCGATTTCAAA 355
QY 238 CTTTACAGCATCGGCGGTCGCGCATTTAGCACTTCGACACCCCATCGCCGCTCAACCG 297
Db 356 CTTTACAGCATCGGCGGTCGCGCATTTTAGCACTTCGACACCCCATTCGCCCGCTCAACCG 415
QY 298 TATCTCGGCGCGCTTGAGCGCTCAACCGCGCTCCGTCGACTTGGGGCGGACGACAGC 357
Db 416 TATCTCGGCGCGCTTGAGCGCTCAACCGCGCTCCGTCGACTTTAAACGGAGCGACAGC 475
QY 358 TTCAGCAAACTCCATCGCGCTTCGCGTATTGAAGGGCGTAAAGCTATGCGTTACCCCG 417
Db 476 TTCAGCAAACTCCACCGCGCTTCGCGTATTGGGGCGTAAAGCTATGCGTTACCCCG 535
QY 418 ATGTGCGATTGATGCGCGCTACCGCTACACTCAACTACATCGGCAAGTCAAGCTGTCAA 477
Db 536 ATGTGCGATTGATGCGCGCTACCGCTACACTCAACTACATCGGCAAGTCAAGCTGTCAA 595
QY 478 AAGTCCGTTCCGCGCACTGTCCGTCGCGGTCGCGTCAAAATTCGA 525
Db 596 AATGTCGTTCCGCGCACTGTCCGCGCGGTACGCGTCAAAATTCGA 643

RESULT 6

US-09-614-912-175
; Sequence 175, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Cairni, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 175
; LENGTH: 1919
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-614-912-175

Query Match 9.5%; Score 49.8; DB 3; Length 1919;
Best Local Similarity 49.8%; Pred. No. 0.001;
Matches 126; Conservative 0; Mismatches 127; Indels 0; Gaps 0;
QY 125 CTGCCAAGGCTTCAGCCGCGCGCATCTCGCAGGCTACCGCATCAACGACCTCCGCGTTGG 184
Db 396 CCGCCTACCGCGCTTCCTCACCATGCGGAGCCACCTGGAGACCAACGTCCTACTCGC 455

RESULT 7

US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 8.7%; Score 45.6; DB 3; Length 4403765;
Best Local Similarity 44.6%; Pred. No. 0.14;
Matches 180; Conservative 0; Mismatches 224; Indels 0; Gaps 0;
QY 10 GCATTTGCCACACTGATTGCTCTCCGCGCGCGGCTCTCCGCGCGCGGACTCGCGGAAAGCGCATCC 69
Db 3731458 GCGTTGCGCGCTTGCGTT 3731517
QY 70 GCTTTTACGTCCAAAGCGATGCCGACACAGCAAAAGCTCAAGCTCTTTAGTTCTGCGC 129
Db 3731518 GCGCGCGCGCGCGCGCTTGCGCGCGGAGCGCGCATTTGCTTGGGGCGCTCCCGGACCGCGC 3731577
QY 130 AAAGGCTTCAGCCCGCGCATCTCCGCGAGCTACCGCATCAACGACTTCGCTTCGCGCGCTC 189
Db 3731578 GTAGCGCGGTTGC 3731637
QY 190 GATTACAGCGCTACAAAACCTATAAAGCCCGCATCCACGATTTCAAACTTTACAGCATC 249
Db 3731638 GAGCGCGCGTTGCGCGCTTAAGAAATGCGCGCACCGCGCTACCGCGCGCTT 3731697
QY 250 GCGCGGTCCGCATTTAGACTTCGACACCCCATTCGCGCGTCAACCGCTATCTCGCGCGC 309
Db 3731698 GCGCGCTGCGCGCTTCCCGCGCATCGCGCTTGGCGCGCGGAGCGCGCGCGCGCGCGC 3731757
QY 310 CGCTTGAGCTCAACCGCGCTCTCCGTCGACTTGGCGCGCGAGCGAGCTTCAGCCAAAC 369
Db 3731758 GGCACCGCGCTCCCGC 3731817
QY 370 TCCATCGCGCTCGCGGTATTGACGGGCGTAAAGCTATGCGGTTCAC 413

QY 133 GGCCTCAGCCCGGATCTCCGAGGCTACCGGATCAAGCACTCCGCTTCGCCGTCGAT 192
 DB 426913 GGCATCTGGCTGACCGGCGACGGCTTGTCCGGCTTCAGCTCCCTGAACCTCCGCGCCCGC 426854
 QY 193 TACACGCGCTACAAAACCTATAAAGCCCATCCACCGATTTCAAACTTTACAGCATCGGC 252
 DB 426853 AACACCGGCTTCTCACTCCGGGACCGGCAACACCGGCTTGTCACTCCGGGACCGGC 426794
 QY 253 GCGTCCGCAATTTACAGCTTCGACACCCCAATCCCGCTCAAAACCGATATCTCGGCGCGGC 312
 DB 426793 AACACCGGCTTGTCACTCCGGGACCGGCAACCGTCCGCAACATGGGCAACCGGC 426734
 QY 313 TTGAGCCTCAACCGCGCTCCGTCAGCTTGGGCGGAGGAGAGCTTCAGGCCAACTCC 372
 DB 426733 GCGTTCCGCGTCCGGCTATCCGGGCGACAGCCAGGTGGGCATCGGCGGCACTCCGCGC 426674
 QY 373 ATCCGCTCCGGCTATTGACGGGCGTAACTATGCGTTTACCCCGAATGTCGATTTGGAT 432
 DB 426673 AGTTTCAACATCGGCTTGTAACTTCGGGACCGGCAATGTCGGCATCGGCACTCGGC 426614
 QY 433 GCGGCTACCGCTACAACTACATCGGCAAGGTCAACACTGTCAAAAAGTTCGTTCCGCGC 492
 DB 426613 ACCGGCAAGCTCGGCATCGGCAACACCGGCACCGGCAACCGGCATCGGCAACCGGC 426554
 QY 493 GAACTGTCGTCGGCGTGGC 513
 DB 426553 AACTACAACACCGGCTTGCTC 426533

RESULT 11
 US-09-881-165-4
 ; Sequence 4, Application US/09881165
 ; Patent No. 6632930
 ; GENERAL INFORMATION:
 ; APPLICANT: HOOD, ELIZABETH
 ; APPLICANT: HOWARD, JOHN
 ; APPLICANT: BAILEY, MICHELE
 ; APPLICANT: GASTEL, FRANS VAN
 ; APPLICANT: WANG, HUAMING
 ; APPLICANT: WARD, MICHAEL
 ; APPLICANT: WOODARD, SUSAN
 ; TITLE OF INVENTION: METHOD OF INCREASING RECOVERY OF HETEROLOGOUS ACTIVE
 ; FILE REFERENCE: 10032R
 ; CURRENT APPLICATION NUMBER: US/09/881,165
 ; PRIORITY FILING DATE: 2001-06-14
 ; PRIOR APPLICATION NUMBER: 60/211,732
 ; PRIOR FILING DATE: 2000-06-15
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 1082
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA encoding
 ; OTHER INFORMATION: Organophosphate Hydrolase
 US-09-881-165-4

Query Match 8.4%; Score 44; DB 3; Length 1082;
 Best Local Similarity 46.0%; Pred. No. 0.03;
 Matches 149; Conservative 0; Mismatches 175; Indels 0; Gaps 0;
 QY 31 CTGCTCTCCCGCGCGCACTGCGGAGGCGCATCGGCTTTTATGTTCAAGCGCAT 90
 DB 522 CTCGTGCTCAAGGCGCGCGCGCTCCCTCCGCAACCGGCTCGCGGTGACCCAC 581
 QY 91 GCGGCACACGAAAGCGCTCAAGCTCTTTAGGTTCTGCGCAAGGCTTCAGCCCGGCGATC 150
 DB 582 ACCGCGGCTCCAGCGGCAAGCGGAGGCGGCGCATCTTCAGTTCGAGGGGCTC 641
 QY 151 TCCGAGGCTACCGCATCAACGACTTCGCGCTTCGCTCGATTCAGCGGCTTACAAAAC 210

DB 642 TCCCGTCCCGGCTGTGATCGGCATCGGCATCCGAGGACACGAGGACCTCTCTTACCTCACC 701
 QY 211 TATAAGGCCCATTCACCGATTTTCAAACTTTTACAGCATCGGCGGCTCCGCCATTTTACGAC 270
 DB 702 GCGCTCGCGCGCGGCTTACTCTCATCGGCTTCGACACATCCGCACTTCGCGCATCGGC 761
 QY 271 TTGACACCAATCGCCGCTCAAAACCGATATCTCGGCGGCGGCTTACGCTCAACCGCGC 330
 DB 762 CTCGAGGACAAAGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCATCGGCTCTTGGCAGACCGCGCC 821
 QY 331 TCCGTGCACTTGGGCGGCGAGGAC 354
 DB 822 CTCCTCATCAAGGCCCTCATCGAC 845

RESULT 12
 US-08-961-527-363
 ; Sequence 363, Application US/08961527
 ; Patent No. 6420135
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles Kunsch
 ; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
 ; NUMBER OF SEQUENCES: 391
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 ; COMPUTER: HP Vectra 486/33
 ; OPERATING SYSTEM: MSDOS version 6.2
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/961,527
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brookes, A. Anders
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PB340P1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 363:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4483 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 US-08-961-527-363

Query Match 8.4%; Score 44; DB 3; Length 4483;
 Best Local Similarity 47.3%; Pred. No. 0.047;
 Matches 174; Conservative 0; Mismatches 185; Indels 9; Gaps 1;
 QY 134 GCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGCTTCGCGCTCGATT 193
 DB 2659 GCTTCAGCAAGTACCAGTGGCTTCGAGCATCAACGAGTGTTCAGTCTCAGCGTCA 2718
 QY 194 ACAGCGGTCAAAAACCTATTAAGCCCATCCACCGATTTCAAACTTTACAGCATCGGG 253
 DB 2719 ACCAGTGCTCTGAATCAGCATCAACAGTGCCTCGGCTTCAGCAAGCACCAGTGCCTG 2778
 QY 254 GTCGCGCATTTA-----CGACTTCGACACCCCAATCGCCGTCACAAACGATATCG 304
 DB 2779 GCTTCAGCAAGTACTAGTGCATCGGCTTCAGCATCGAAGTGCCTGTGAATCGGCATCA 2838

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Total number of hits satisfying chosen parameters: 12077628

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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8: /cgm2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2.*
9: /cgm2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3.*
10: /cgm2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	502.6	95.7	710	7	US-11-103-957-91
2	480.2	91.5	525	6	Sequence 91, Appli
3	368	70.1	486	6	Sequence 2511, Ap
4	45.6	8.7	4617	7	Sequence 5309, Ap
5	45	8.6	9903	7	Sequence 530, App
6	44.4	8.5	687	6	Sequence 517, App
7	44.2	8.4	1659	7	Sequence 1753, Ap
8	43.8	8.3	708	6	Sequence 552, App
9	43	8.2	558	6	Sequence 2385, Ap
10	43	8.2	687	6	Sequence 7853, Ap
11	43	8.2	696	6	Sequence 6237, Ap
12	43	8.2	714	6	Sequence 5651, Ap
13	43	8.2	3990	7	Sequence 6247, Ap
14	42.8	8.2	567	6	Sequence 520, App
15	42.6	8.1	4983	7	Sequence 3183, Ap
16	41.2	7.8	843	6	Sequence 521, App
17	41.2	7.8	843	6	Sequence 7073, Ap
18	40.8	7.8	4146	7	Sequence 8005, Ap
19	40.6	7.7	834	6	Sequence 522, App
20	40.6	7.7	6210	7	Sequence 6725, Ap
21	40.4	7.7	681	6	Sequence 1, Appli
22	40.4	7.7	681	6	Sequence 53, Appli
23	40.4	7.7	795	6	Sequence 829, App
					Sequence 1777, Ap

24	40.4	7.7	834	6	US-10-467-657-7385	Sequence 7385, Ap
25	40.4	7.7	939	6	US-10-467-657-7399	Sequence 7399, Ap
26	40.4	7.7	3711	6	US-10-873-528-321	Sequence 321, App
27	39.4	7.5	5706	7	US-11-052-554A-519	Sequence 519, App
28	39.2	7.5	2562	7	US-11-052-554A-533	Sequence 533, App
29	39	7.4	1280	6	US-10-802-796-4	Sequence 4, Appli
30	39	7.4	2406	7	US-11-052-554A-550	Sequence 550, App
31	39	7.4	88421	7	US-11-205-109-1	Sequence 1, Appli
32	38.8	7.4	1650	6	US-10-858-730-140	Sequence 140, App
33	38.4	7.3	5706	7	US-11-052-554A-519	Sequence 519, App
34	38.2	7.3	678	6	US-10-467-657-6037	Sequence 6037, Ap
35	38.2	7.3	1632	7	US-11-052-554A-546	Sequence 546, App
36	38.2	7.3	3240	7	US-11-052-554A-529	Sequence 529, App
37	38	7.2	2196	7	US-11-052-554A-539	Sequence 539, App
38	38	7.2	2277	6	US-10-467-657-2721	Sequence 2721, Ap
39	38	7.2	6615	7	US-11-052-554A-518	Sequence 518, App
40	37.2	7.1	888	6	US-10-858-730-183	Sequence 183, App
41	37.2	7.1	1497	6	US-10-467-657-2095	Sequence 2095, Ap
42	37.2	7.1	1821	7	US-11-052-554A-547	Sequence 547, App
43	36.6	7.0	2205	6	US-10-467-657-3729	Sequence 3729, Ap
44	36.6	7.0	2205	6	US-10-467-657-6989	Sequence 6989, Ap
45	36.6	7.0	2337	7	US-11-052-554A-528	Sequence 528, App

ALIGNMENTS

RESULT 1
US-11-103-957-91
; Sequence 91, Application US/11103957
; Publication No. US20050281847A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Verlant, Vincent Georges Christian Louis
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45261
; CURRENT APPLICATION NUMBER: US/11/103,957
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: US/10/467,534
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/EP02/01356
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103169.9
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 710
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-11-103-957-91
Query Match 95.7%; Score 502.6; DB 7; Length 710;
Best Local Similarity 97.3%; Pred. No. 2.1e-125;
Matches 511; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 ATGAAAAAGCATTGCCACACTGATTCCTCCCTCGCTCTCCGCGCGCGCGCGCGGAA 60
DB 141 ATGAAAAAGCATTGCCACACTGATTCCTCCCTCGCTCTCCGCGCGCGCGCGCGGAA 200
QY 61 GGCGCATCCGCTTTTACGTCCAAAGCCGATCCGCGCACACGCAAAAGCTCTCAAGCTCTTTA 120
DB 201 GGCGCATCCGCTTTTACGTCCAAAGCCGATCCGCGCACACGCAAAAGCTCTCAAGCTCTTTA 260
QY 121 GGTTCGCAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACTTCGCG 180
DB 261 GGTTCGCAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACTTCGCG 320
QY 181 TTGCGCGTCGATTACACGCGCTTACAAAACCTATAAAGCCCATCCACCGATTTCAACTT 240
DB 321 TTGCGCGTCGATTACACGCGCTTACAAAACCTATAAAGCCCATCCACCGATTTCAACTT 380

QY 241 TACAGCATCGGCGGTCCGCGCATTTACGACTTCGACACCCCAATCCCGGTCAAAACCGTAT 300
DB 381 TACAGCATCGGCGGTCCGTCATTTACGACTTCGACACCCCAATCCCGGTCAAAACCGTAT 440
QY 301 CTCGGCGCGCTTGAGCCTCAACGGCGCTCCGTCGACTTGGGCGGAGCGACAGCTTC 360
DB 441 TTCGGCGCGCTTGAGCCTCAACGGCGCTCCGCGCCACTTGGGCGGAGCGACAGCTTC 500
QY 361 AGCCAAACCTCCATCGGCTCGGCGTATTTGACGGCGGTAAAGCTATGCGTTACCCCGAAT 420
DB 501 AGCAAAACCTCCGCGGCTCGGCGTATTTGCGGCGGTAAAGCTATGCGTTACCCCGAAT 560
QY 421 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAC 480
DB 561 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAC 620
QY 481 GTCGCTTCCGCGCAACTGCTCGGCGGTGCGGTGCGGTCAAAATCTGA 525
DB 621 GTCGCTTCCGCGCAACTGCTCGGCGGTGCGGTGCGGTCAAAATCTGA 665

RESULT*2
US-10-467-657-2511
; Sequence 2511, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2511
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2511

Query Match 91.5%; Score 480.2; DB 6; Length 525;
Best Local Similarity 96.0%; Pred. No. 2e-119;
Matches 504; Conservative 0; Mismatches 18; Indels 3; Gaps 1;
QY 1 ATGAAAAAGCATTGCCACACTGATTCGCTCTCCGCGCGCGCGCACTGCGGAA 60
DB 1 ATGAAAAAGCATTGCCACACTGATTCGCTCTCCGCGCGCGCGCACTGCGGAA 60
QY 61 GCGGCATCCGCTTTTACGTCGAAGCGGATGCGGCACACGCAAAAGCCTCAAGCTCTTTA 120
DB 61 GCGGCATCCGCTTTTACGTCGAAGCGGATGCGGCACACGCAAAAGCCTCAAGCTCTTTA 120
QY 121 GGTTCGCAAGGCTTACGCGCGGCTACCGAGGCTACCGGATCAACGACTTCGC 180
DB 121 GGTTCGCAAGGCTTACGCGCGGCTACCGAGGCTACCGGATCAACGACTTCGC 180
QY 181 TTGCGGTGCGATTAACGCGGTACAAAACCTATATAAAGGCGCCATCCCGATTTCAA 237
DB 181 TTGCGGTGCGATTAACGCGGTACAAAACCTATATAAAGGCGCCATCCCGATTTCAA 240
QY 238 CTTTACAGCATCGGCGCTCCGCCATTTACGACTTCGACACCCCAATGCCCGTCAAAACCG 297
DB 241 CTTTACAGCATCGGCGCTCCGCCATTTACGACTTCGACACCCCAATGCCCGTCAAAACCG 300
QY 298 TATCTCGCGCGCGCTTACGCTCAACCGCGCTCCGTCGACTTGGGCGGAGCGACG 357
DB 301 TATTTGCGCGCGCTTACGCTCAACCGCGCTCCGTCGACTTGGGCGGAGCGACG 360

QY 358 TTCAGCCAAACCTCCATCGGCTCGGCGTATTTGACGGCGGTAAAGCTATGCGTTACCCCG 417
DB 361 TTCAGCCAAACCTCCGCGCGCTCGGCGTATTTGCGGCGGTAAAGCTATGCGTTACCCCG 420
QY 418 AATGTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAA 477
DB 421 AATGTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAA 480
QY 478 AAGTCCGTTCCGCGCAACTGCTCGGCGGTGCGGTCAAAATTC 522
DB 481 AAGTCCGTTCCGCGCAACTGCTCGGCGGTGCGGTCAAAATTC 525

RESULT 3
US-10-467-657-2509/c
; Sequence 2509, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2509
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2509

Query Match 70.1%; Score 368; DB 6; Length 486;
Best Local Similarity 95.6%; Pred. No. 2.1e-89;
Matches 390; Conservative 0; Mismatches 15; Indels 3; Gaps 1;
QY 121 GGTTCGCCAAAGGCTTACGCGCGCATCTCCGAGGCTACCGCATCAACGACTTCGC 180
DB 486 GGTTCGCCAAAGGCTTACGCGCGCATCTCCGAGGCTACCGCATCAACGACTTCGC 427
QY 181 TTGCGCGTCAATACAGCGCTACAAAACCTATA--AAGCCCATCCACGATTTCAA 237
DB 426 TTGCGCGTCAATACAGCGCTACAAAACCTATAAACAAGCCCATCCACGATTTCAA 367
QY 238 CTTTACAGCATCGGCGGTCCGCCATTTACGACTTCGACACCCCAATGCCCGTCAAAACCG 297
DB 366 CTTTACAGCATCGGCGGTCCGTCATTTACGACTTCGACACCCCAATGCCCGTCAAAACCG 307
QY 298 TATCTCGCGCGCGCTTTAGCCTCAACCGCGCTCCGTCGACTTGGGCGGAGCGACG 357
DB 306 TATTTGCGCGCGCTTTAGCCTCAACCGCGCTTCCGCCCATCTTGGGCGGAGCGACG 247
QY 358 TTGAGCAAAACCTCCATCGGCGCTCGGCGTATTTGACGGCGGTAAAGCTATGCGTTACCCCG 417
DB 246 TTGAGCAAAACCTCCGCGCGCTCGGCGTATTTGCGGCGGTAAAGCTATGCGTTACCCCG 187
QY 418 AATGTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAA 477
DB 186 AATGTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAA 127
QY 478 AAGTCCGTTCCGCGCAACTGCTCGGCGGTGCGGTCAAAATCTGA 525
DB 126 AAGTCCGTTCCGCGCAACTGCTCGGCGGTGCGGTCAAAATCTGA 79

RESULT 4
US-11-052-554A-530/c

```
; Sequence 530, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; PRIOR FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 530
; LENGTH: 4617
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-530

Query Match      8.7%; Score 45.6; DB 7; Length 4617;
Best Local Similarity 44.6%; Pred. No. 0.007;
Matches 180; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

Qy 10 GCACCTGACACATGATTCCTCTCCCGCGCGCGCGCTCCCGCGCACATGCGCGAAGCGCATCC 69
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 70 GGCTTTTACGTCAAGCCGATGCGCACACGGAAGAGCTCAAGCTCTTTAGTTCCTGCC 129
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3546 GCCCGCGCGCGCGCTTTCGCGCGAGCGCGCATTTGCGCTTTCGCGCGCTCCCGGACCGCC 3487
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 130 AAAGCTTTCAGCGCGCATCTCGCGAGCTACGCGATCAAGACCTCGCTTTCGCGCTC 189
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3486 GTAGCGCGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3427
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 190 GATTACACGCGCTACAAAATATATAAGCGCCCATCCACCGATTTTCAAACTTTACAGCATC 249
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3426 GAGCGCGCGCTTTCGCGCGCTAGGAATGCGCGCCCGCGCGCGCGCGCGCGCGCGCT 3367
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 250 GCGCGCTCGCGCATTTAGACTTCGACACCCATCGCGCGTCAAAACCGTATCTCGCGCG 309
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3366 GCGCGCTGTGCGCGCTTCCCGCGCGATGCGCGCTTGGCGCGCGAAGCGCGCGCGCGCC 3307
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 310 CGCTTGACCTCAACGCGCGCTTCGCTGCACTTGGCGCGCGAGCGAGCTTCAGCCARACC 369
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3306 GGCACCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3247
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 370 TCCATCGCGCTCGCGGTATTGACGGCGGTAAAGCTATGCGGTAC 413
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3246 GCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3203
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
US-11-052-554A-517
; Sequence 517, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; PRIOR FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 517
; LENGTH: 9903
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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-517

Query Match      8.6%; Score 45; DB 7; Length 9903;
Best Local Similarity 44.9%; Pred. No. 0.012;
Matches 171; Conservative 0; Mismatches 210; Indels 0; Gaps 0;

Qy 133 GGCTTTCAGCGCGCATCTCCGCGAGGTACCGCATCAACGACCTCCGCTTCGCGCTCGAT 192
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 7765 GGCATCTGGCTGACCGCGGCGGCTTGTCCGGCTTCAGTCCCTGAACTCCGCGCGCGCG 7824
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 193 TACAGCGCTACAAAACATAAAGCCCATCCACCGATTTCAAACTTTACAGCATCGCG 252
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 7825 AACACCGGTTTCTTCAACTCCGCGCACCGCCCAACACCGGCTTTGTTCAACTCCGCGCACCGCGC 7884
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 253 GCGTCCGCGCATTTAGACTTCGACACCGCAATCGCCCGTCAAAACCGTATCTCGCGCGCGCGC 312
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 7885 AACACCGGCTTGTCAACTCCGCGCACCGGCAACGTCGCGCATCGGCAACATGGGCAACCGCGC 7944
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 313 TTGAGCCTCAACCGCGCTCCGTCGACTTGGCGCGGACGCAAGCTTCAGCCAAACCTCC 372
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 7945 GCGTTTCGCGCTGCGCTATCCGCGCACAGCGAGGTGGCGCATCGCGCGCACCAACTCGCGC 8004
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 373 ATCGCGCTCGCGGTATTGACGCGGGGTAAAGCTATGCGGTTACCCCGAATGTCGATTTGAT 432
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 8005 AGTTTCAACATCGCGCTTGTTTAACTCGCGCACCGGCAATGTCGCGCATCGGCAACTCGCGC 8064
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 433 GCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAACGTCGTTCCGCGC 492
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 8065 ACCGCAACGTGCGCATCGGCAACACCGGCAACCGGCAACCGGCAACCGGCAACGAGCGCGC 8124
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 493 GAACTGTCTCGCGCGCTGCGC 513
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 8125 AACTACAACCGGCTTGCTC 8145
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
US-10-467-657-1753
; Sequence 1753, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1753
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1753

Query Match      8.5%; Score 44.4; DB 6; Length 687;
Best Local Similarity 64.7%; Pred. No. 0.0094;
Matches 66; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 351 GCACAGCTTCAGCCAAACCTCCATCGCGCTCGGCGTATTGACGGCGTAAAGCTATGCGGT 410
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 519 CGAAAGCGCGACGAGCGCGCTTGGGCTTCGCGCGATGCGGCGGTGGGCGGTAGACGT 578
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 411 TACCCCGAATGTCGATTTGGATGCGGCTACCGCTTACAACTA 452
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 579 GCGCGCGGCTGACCTTGGACCGCGGCTACCGCTACCACCTA 620
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```

RESULT 7
US-11-052-554A-552
; Sequence 552, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 552
; LENGTH: 1659
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-552

```

	Query Match	8.4%; Score 44.2; DB 7; Length 1659;
	Best Local Similarity	45.3%; Pred. No. 0.013;
	Matches 160; Conservative 0; Mismatches 193; Indels 0; Gaps 0;	
Qy	129 CAAAGGCTTCAGCCCGGCATCTCCGAGGCTACCGCATCAAGACCTTCGGTTCGCGGT	188
Db		
Qy	588 CACGGCAGCGGCAACATCGGCACCGGAAACAAAGGCAAGTCTCCAACTTCGGCGCGGCA	647
Db		
Qy	189 CGATTACACGGCTTACAAAACCTATAAAGGCCCATCCACCGATTTCAAACTTTACAGCAT	248
Db		
Qy	648 CATCGGCATTAACAACATCGGCAGCGGCACCGAGGACGCAACCTTCGGCGCGGCA	707
Db		
Qy	249 CGGCGCTTCGGCCATTTACGACTTTGCAACCCCAATCGCCGTCGTCAAAACGCTATCTTCGGGCG	308
Db		
Qy	708 CGTCGGCACCGGAAACATCGGCTTCGGCAACCGAGGGCCCCATAGACGTTAACTCTTTGGC	767
Db		
Qy	309 GCGCTTGAGCTCAACCGCGCCTTCGTCGACTTGGGGGGCAGCGACAGCTTCAGCCCAAC	368
Db		
Qy	768 GACCCGGGCGAACAACGCTGGGCGCTTCGGGCAACATCGGCACCAACCAATGGGCTTCGG	827
Db		
Qy	369 CTCATTCGGCCTTCGGCGCTATTGACGGCGCTAAGCTATGTCGCTTACC CGGAATGTCGATTT	428
Db		
Qy	828 CAACACGGCGACGCGCAACACCGGCGGGCGCAACACCGGCNAACGGCAACATCGTGGCGG	887
Db		
Qy	429 GGAATCGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAACG	481
Db		
Qy	888 CAACACCGGCAACAACTTTTCGGCTTCGGCAACCGGCAACCAACCAACATCG	940
Db		

```

RESULT 8
US-10-467-657-2385
; Sequence 2385, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2385
; LENGTH: 708
;

```

```

; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2385

Query Match      8.3%; Score 43.8; DB 6; Length 708;
Best Local Similarity 47.0%; Pred. No. 0.014;
Matches 135; Conservative 0; Mismatches 152; Indels 0; Gaps 0

Qy 170 ACGACCTTCGCTTCGCCGTGCAATTACACGGCGCTACAAATACTATAAGAGCCCATCCACCG 229
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 278 ACGACGCCGTACGCCCAAGACACCACTCTCTTCGACGGGCTGAACGAACATCATCGCG 337

Qy 230 ATTTCAAACCTTTTACAGCATCGGCGCGTCGCGCAATTTACGACTTCGACACCCAAATGCGCCG 289
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 338 AACTCGACAGACGGGCATCAAAATGGGGCATCATCAACAACCAACCATGCGTTCACCG 397

Qy 290 TCAAAACGATATCTCGGCGCGGCTTGAGCCCTCAACCGCGGCTCGTCGACATTTGGGCGGCA 349
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 398 ACAAACTCGTTCCTCCAAACTCGGAATTCGCCGTTTCGCCCGGCACCGTCGTACAGCGGCGACA 457

Qy 350 GCGACAGCTTCAGCGAAACCTTCATCGCCCTCGCGCTATTGACGGGCGGTAACTATGCGG 409
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 458 CTTGGCGGAACCCAAACCCAGCATCAAAACCATGCTGCACGCTCGGGAATAATCCACG 517

Qy 410 TTATCCCGGAATGCGATTTTGGATTCGCGGCTTACCGGCTTAACTACATC 456

Db 518 CCGACCGGCAACACACCCCTCTAGTCGGCGACGGCGGAACGCGCATC 564

```

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RESULT 9
US-10-467-657-7853
; Sequence 7853, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 7853
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7853

```

Query Match	8.2%	Score 43;	DB 6;	Length 558;
Best Local Similarity	69.94;	Pred. No. 0.021;		
Matches 58;	Conservative 0;	Mismatches 25;	Indels 0;	Gaps 0;

Qy	248	TCGCGCGCTCCGCCATTACGACTTGACACCCCAATCGCCGTCACAAACCGTATCTCGGCG	307
Db	191	TCGCGCTTGTCCGCGGTTTACGATTTTCGATACCGGTTCCCGCTTCAAACCCCTATCAGGCG	250
Qy	308	CGCGCTTGGACCTCAACCGCGCC	330
Db	251	TGCGCGTCACTACGGACACGTC	273

RESULT 10

US-10-467-657-6237

; Sequence 6237, Application US/10467657

; Publication No. US20050260581A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON SpA

; APPLICANT: FONTANA Maria Rita

```

; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6247
; LENGTH: 714
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-6247

```

	Query Match	8.2%	Score 43;	DB 6;	Length 714;
	Best Local Similarity	62.6%;	Pred. No. 0.023;		
	Matches 67;	Conservative 0;	Mismatches 40;	Indels 0;	Gaps 0;
Qy	352	GACAGCTTCAGCCAAACCTCCATCGGCTCGGCGTATTGACGGCGCTAAGCTATGCGGTT	411		
Db	210	GAAGGACAGCATCCGCCCGCTCGGCGTATCGCGCGCTCGGTTTCGATC	151		
Qy	412	ACCCGGAATGCGATTGGATGCGCGGTACCGCTACCACTACATCGG	458		
Db	150	ACGCCCAACTGACCTTGGACGCGCGGTACCGCTACCACTACGCGG	104		

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RESULT 13
US-11-052-554A-520/c
; Sequence 520, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 520
; LENGTH: 3990
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-520

```

	Query Match	8.2%	Score 43;	DB 7;	Length 3990;
	Best Local Similarity	42.9%;	Pred. No. 0.034;		
	Matches 214;	Conservative 0;	Mismatches 285;	Indels 0;	Gaps 0;
Qy	10	GCATTGGCCACACTGATTGGCTCTCCCGCGCGCCGCACTGGCGGAAGGGCGCATCC	69		
Db	1929	GCATTACCAACAAAGCCCGCTTGGCGCCCTTGGCGCGCGCCGCGCCCGCCCGCCGCGC	1870		
Qy	70	GGCTTTTACGTCGAAGCCGATGCGGCACACGCAAAAAGCTTCAAGCTCTTTAGGTTCTTGCC	129		
Db	1869	GACGGTGGCGTTTCGCGCGGTTGCGCGCGGTGCGCGCGCTTGC CGCGCTGGTTCGGGGTGGC	1810		
Qy	130	AAAGGCTTCAGCCGCGGCATCTCGGAGGCTACGGATCAACGACCTCCGCTTCGCGCGTC	189		
Db	1809	GCCGCGGGCACCGTCTTGACCCCGCGGTGGATTCGGCGCCCGCATCCACAGCACCAACC	1750		
Qy	190	GATTACACGCGCTACAAAAACTATAAGCCCCCATCCACCGATTTCAAACTTTTACAGCATC	249		
Db	1749	GATGCGCGGCTACTCGCGGTTGCGCGCGTTGCGCAACCAACTCCATCGCGCGGTTATCGAA	1690		

150	AAAGGGGTTGAGCCCGGCGCATCTTCGAGGGATCCATCATGAGGACCTCCCGCTAGCGGCTC	169
QY		
1809	GCCGCGGGCACCGTCTGTCACCCCGGTGGATCGGGCGCCCGGATCCACCGACGACCACC	1750
Db		
190	GATTACACGGCGTCAAAAACCTATAAAGCCCCATCCACCGATTTTCAAACTTTACAGCATC	249
QY		
1749	GATGCGCGGCGCTACCGCCGTTGCGCGCGTTGGCAACCACTTCCATCGCGCGCGTTATCGAA	1690
Db		

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2006, 19:58:14 ; Search time 3281 Seconds
(without alignments)
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Title: US-10-650-123-1
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Searched: 41078325 seqs, 23393541228 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
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5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsa1:*
10: gb_gsa2:*
11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57.8	11.0	622	6	CA197724 SCAGAD107
2	56.4	10.7	626	6	CA193415 SCCFL100
3	55.2	10.5	787	6	CB654660 OSJNEC07F
4	54.2	10.3	743	10	C2247380 AIAA-aaif3
5	53.6	10.2	591	6	CB640993 OSJNEal7F
6	53.6	10.2	665	7	CV152413 LS245-S-8
7	53.6	10.2	698	6	CB653730 OSJNEC05A
8	53.6	10.2	725	6	CB677411 OSJNEal4E
9	53.6	10.2	741	6	CF589226 EST00F06
10	53.6	10.2	759	6	CB671800 OSJNEe05I
11	53.6	10.2	762	6	CB677339 OSJNEal4C
12	53.6	10.2	775	6	CB677062 OSJNEal3K
13	53.6	10.2	778	6	CB654692 OSJNEC07G
14	53.6	10.2	782	6	CB665147 OSJNEdl1F
15	53.6	10.2	842	6	CB668023 OSJNEdl5K
16	53.4	10.2	561	6	CF278525 14ETL--04
17	53.4	10.2	644	6	CF315326 HD--04-D0
18	52.2	9.9	525	6	CF308604 ABF--02-H
19	52	9.9	696	6	CD935542 OV.101M15
20	51.8	9.9	530	6	CF335206 JMT--04-M
21	51.8	9.9	558	2	BG560231 RH122_71
22	51.8	9.9	655	6	CA172233 SCSPFSB107

23	51.8	9.9	693	6	CA253038	SCJLPLA09
24	51.8	9.9	773	6	CA231223	SCQSL303
25	51.8	9.9	1182	8	DN655133	CEC15-C02
26	51.2	9.8	519	7	CV097296	FAMU USDA
27	50.8	9.7	691	9	BH898151	MB61P2A7
28	50.6	9.6	649	6	CD219573	CCCL_57_A
29	50.6	9.6	666	6	CD222538	CCCL_22_G
30	50.6	9.6	669	6	CD222866	CCCL_24_B
31	50.2	9.6	744	6	CB681064	OSJNEf06N
32	50.2	9.6	1170	10	CL978445	CL978445 OsIFCC031
33	50.2	9.6	2397	10	CL973983	CL973983 OsIFCC025
34	50	9.5	670	3	BJ748832	BJ748832 OsIFCC021
35	49.8	9.5	2667	10	CL971648	CL971648 OsJNEB04J
36	49.2	9.4	881	6	CB643751	OSJNEB04J
37	49.2	9.4	1196	7	CK167632	FGAS05203
38	49	9.3	515	2	BG560157	BG560157 RH122_71
39	49	9.3	645	1	AJ389106	AJ389106 GH20192_5
40	49	9.3	662	6	CD223038	CCCL_25_B
41	48.8	9.3	559	1	AM680997	WS1_9_E10
42	48.8	9.3	567	2	BE593027	WS1_93_D1
43	48.8	9.3	620	2	BE357605	DGI_21_E0
44	48.8	9.3	658	6	CD463595	ETH1_45_P
45	48.8	9.3	709	10	CW197767	CW197767 104_622_1

ALIGNMENTS

RESULT 1
CAL197724
LOCUS SCAGAD1074C04.g AD1 Saccharum officinarum cDNA clone SCAGAD1074C04
DEFINITION 5', mRNA sequence.
ACCESSION CAL197724
VERSION CAL197724.1 GI:35228269
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
REFERENCE 1 (bases 1 to 622)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,B.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parvada@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.uneep.br>
Plate: 074 row: C column: 04
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1..622
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCAGAD1074C04"
/lab_host="DH10B"
/clone_lib="AD1"

note="Organ: seedlings inoculated with Gluconacetobacter diazotrophicans; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [seedlings inoculated with Gluconacetobacter diazotrophicans]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose

CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>

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ORIGIN
Query Match      11.0%; Score 57.8; DB 6; Length 622;
Best Local Similarity 47.4%; Pred. No. 5.3e-05;
Matches 173; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

Qy 27 TGCCTCGCTCTCCGCGCGCGCACTGGCGGAAGGCGCATCCGGCTTTACGTCCAAGC 86
Db 108 TGATCGCTCTCGCGCATCGCATATTCACCGCGGCGCATGCCCGGTGACGCGCAACG 167
Qy 87 CGATGCGCGCACACGCAAAAGCTCAAGCTCTTTAGGTTCGCCAAAGGCTTCACGCCGCG 146
Db 168 CGCCACCGTCCAACTCCCGCGCCCGGCGGCGGCGGCTCAGGCGGCTCCAGGCGCA 227
Qy 147 CATCTCGCGAGGTACCGCATCAACGACCTCCGCTTCGCGGTGATTCACGCGCTACAA 206
Db 228 ACCGCTCTCCCGCGCCACCGCACTCTCCCGGCTCCGACGACGCGGCGGCGGCGG 287
Qy 207 AAATATTAAGCCCGATCCACCGATTTCAAACTTTACAGCATCGCGGGTTCGCGCATTTA 266
Db 288 CACCACCGACACAGCTTTCTCGGCTCCCAACAGCGGCTCCCGCGGCGGCGGCGGCACTC 347
Qy 267 CGACTTGACACCCCAATCGCGCGTCAACCGTATCTCGGCGGCGGCTTGAGCTCAACCG 326
Db 348 CTTCTCCAGCGCCACACACGCGTCTCGGTCAACGTCGCGGCGGCGGCGGCGGCTCCCA 407
Qy 327 CGCTTCGCTGACTTGGCGCGCAGCGACGCTTCAGCGCAACCTTCATCGGCTTCGGGT 386
Db 408 CCACCTCGCTGACGCTCTCCCGCGGTGAGCGCGACACCGGTCGCGGCGGCGGCGGCT 467
Qy 387 ATTGA 391
Db 468 TTCA 472
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RESULT 2
CA193415
LOCUS      626 bp mRNA linear EST 24-SEP-2003
DEFINITION Saccharum officinarum cDNA clone SC0CFL1003E05
5', mRNA sequence.
CA193415
CA193415.1 GI:35140555
EST.
SOURCE      Saccharum officinarum
ORGANISM    Saccharum officinarum
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REFERENCE
1 (bases 1 to 626)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenhariaia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 003 row: E column: 05
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1. .626
/organism="Saccharum officinarum"
/mol_type="mRNA"
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FEATURES
source
/db_xref="taxon:4547"
/clone="SC0CFL1003E05"
/lab_host="DH10B"
/clone_lib="FL1"
/note="Organ: Inflorescence at beginning of development (1cm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from (Inflorescence at beginning of development (1cm-long)). cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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ORIGIN
Query Match      10.7%; Score 56.4; DB 6; Length 626;
Best Local Similarity 47.2%; Pred. No. 0.00013;
Matches 171; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

Qy 27 TGCCTCGCTCTCCGCGCGCGCACTGGCGGAAGGCGCATCCGGCTTTACGTCCAAGC 86
Db 58 TGATCGCTCTCGCGCATCGCATATTCACCGCGGCGCATGCCCGGTGACGCGCAACG 117
Qy 87 CGATGCGCGCACACGCAAAAGCTCAAGCTCTTTAGGTTCGCCAAAGGCTTCAGCGCGCG 146
Db 118 CGCCACCGTCCAACTCCCGCGCCCGGCGGCGGCTCAGGCGGCTCCGCGGCGCA 177
Qy 147 CATCTCGCGAGGTACCGCATCAACGACCTTCGCGGTGATTCACGCGCTACAA 206
Db 178 ACCGCTCTCCCGCGCCACCGCACTCTCCCGGCTCCGACGACGCGGCGGCGGCGG 237
Qy 207 AAATATTAAGCCCGATCCACCGTATTTCAAACTTTACAGCATCGCGGCTTCGCGCATTTA 266
Db 238 CACCACCGACACGCTCTCCCGGCTCCCAACGCGGCGGCGGCGGCGGCGGCGGCGGCTC 297
Qy 267 CGACTTCGACACCCCAATCGCGCGTCAACCGTATCTCGGCGGCGGCTTGAGCTTCACCG 326
Db 298 CTCTCCAGCGCGCCACACCGCGCTCCGTCACCGCGCGGCGGCGGCGGCGGCTCCCA 357
Qy 327 CGCTTCGCTGACTTGGCGCGCAGCGACGCTTCAGCGCAACCTTCATCGGCTTCGGGT 386
Db 358 CCACTCGCGCGGCTCTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 417
Qy 387 AT 388
Db 418 CT 419
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RESULT 3
CB654660
LOCUS      787 bp mRNA linear EST 09-APR-2003
DEFINITION OSJNEC07F21.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEC07F21 5', mRNA sequence.
CB654660
CB654660.1 GI:29658385
EST.
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ACCESSION
VERSION
KEYWORDS
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Oryzaceae; Oryza.
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REFERENCE
1 (bases 1 to 787)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
```

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JOURNAL
PUBMED
COMMENT
Contact: Rod Wing
Arizona Genomics Institute
```

University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 9967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 07 row: F column: 21
Seq primer: gta aaa cga cgg cca gtc.

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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEC07F21"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEC"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2: XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"
ORIGIN
Query Match 10.5%; Score 55.2; DB 6; Length 787;
Best Local Similarity 44.7%; Pred. No. 0.00029;
Matches 213; Conservative 0; Mismatches 263; Indels 0; Gaps 0;

QY 41 CGGCCGCGCACTGCGGAGCGCATCGGGTTTATCGTCAACGCCGATGCGGACACG 100
DB 60 CAGCAGCGCCATGAGGAGATACGACCGCGAGTTCTACAGTTTACCGACGAGTGGCGC 119
QY 101 CAAGAAGCTCAGCTTTAGGTTCTGCCAAGGCTTCAGCCGCGCATCTCGGAGGCT 160
DB 120 TGCAGACGGCGAGCTTCTCCGCGCTCTCCCTCGGAGCTCCATCTGGTCTCCCTCCG 179
QY 161 ACCGCGATCAACGACCTCGCTTCGCGCTGATTTACACGCGCTTACAAAACATATAAGGCC 220
DB 180 ACCGCGGCAACGAGCGCGCTTCGAGCGGAGTACACGACTTCTCTCCCTCCCTCCG 239
QY 221 CATCACCGATTTCAAACTTTACAGATCGGCGCTCGGCCATTTACGATTCGACACCC 280
DB 240 CCAAGAACGCGCATCGCCAACTCAACGCGCTCGCGGAACTCGGATGGCGCGGCTCA 299
QY 281 AATCGCGCTCAACCGTATCTCGGCGCGGCTTGAGCTCAACCGCGCTCGGCTCGACT 340
DB 300 TGGGCTCCGGCAAGCTCGCTTCGCGCGCCACCAAGCGCGACCGCTTACACGCGTCAACC 359
QY 341 TGGGCGGAGGACAGCTTCAGCCAAACCTCCATCGGCTCGGCGTATTGACGGCGGTA 400
DB 360 TCCCGCTGACAAACAAACAAACAAAGTCTACGCGGCGCGCGGAGATCAACAA 419
QY 401 GCTATCGCGTTACCCGGAATTCGATTTGATTCGCGGCTTACGCTTACAACTACATCGGCA 460
DB 420 ACAAGTCAACGCTTCGGGTTCAACAGATGGGGGTTTACAAACAGCAGCAGCAGCG 479
QY 461 AGTCAACACTGTCAAAACGTCCTTCGCGGCACTGCTCGGCGGCTCGGCTCGGCGTC 516
DB 480 GCGGCAACTTACGGCGGCAACGCGCGGAGCTGTAAGAGCTTACTTCAACAGTCCGTC 535

RESULT 4
CZ247380
LOCUS
DEFINITION
AIAA-aaf35a12.b1 Ancylostoma caninum whole genome shotgun library (AIAAGSS 001) Ancylostoma caninum genomic, genome survey sequence.
ACCESSION
CZ247380
VERSION
CZ247380.1
KEYWORDS
GSS.
SOURCE
Ancylostoma caninum (dog hookworm)
ORGANISM
Ancylostoma caninum

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma. 1 (bases 1 to 743)
Mitrevna,M., McCarter,J.P., Pape,D., Ritter,E., Tsagareishvili,R., Ronko,I., Martin,J., Wylie,T., Dante,M., Meyer,R., Messina,D., Waterston,R.H., Clifton,S.W. and Wilson,R.
Genome Survey sequences from the parasitic nematode Ancylostoma caninum
Unpublished (2004)
Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: nematode@watson.wustl.edu
Genomic DNA provided by John Hawdon (mtmjmh@wumc.edu) DNA sequenced by Washington University Genome Sequencing Center
Class: shotgun.

FEATURES
source
1..743
/organism="Ancylostoma caninum"
/mol_type="genomic DNA"
/strain="Baltimore"
/db_xref="taxon:29170"
/dev_stage="Adult"
/lab_host="GS10"
/clone_lib="Ancylostoma caninum whole genome shotgun library (AIAAGSS 001)"
/note="Vector: pOTW13; Site 1: BstXI; Site 2: BstXI; Ancylostoma caninum genomic DNA was randomly sheared, end-repaired and size fractionated to enrich for 2-4 kb fragments. Genomic DNA was provided by John Hawdon (mtmjmh@wumc.edu) at George Washington University. Sequencing by Washington University Genome Sequencing Center, St. Louis, MO."
ORIGIN
Query Match 10.3%; Score 54.2; DB 10; Length 743;
Best Local Similarity 47.0%; Pred. No. 0.00054;
Matches 167; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 129 CAAGGCTTACGCGCGCATCTCGCAGGCTACCGATCAACGACCTCGGCTTCGCGT 188
DB 113 CAACAAACGACAAACAAACGACGACAAACGACAAACGACAAACGACAA 172
QY 189 CGATTACAGCGCTACAAACTATAGCCCATCCACCGATTTCAACTTTACGAT 248
DB 173 CAACAAACAAACAAACAAACGACGACAAACGACAAACGACGACAAACAA 232
QY 249 CGGCGGCTCGGCGCATTTACGACTTCGACACCAATCGCGCTTATCTCGGCGC 308
DB 233 CAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 292
QY 309 GCGCTTGAGCTCAACCGCGCTCGCTCGACTTGGGCGGCGGAGGAGCTTCAGGCAAC 368
DB 293 CAACGACAAACAAACGACGACGACGACGACGACGACGACGACGACGACGAC 352
QY 369 CTCCATCGGCTCGGCGTATTGACGGGCTGAGCTATCGGCTTACCCGAGTGTGATT 428
DB 353 CAACAAACAAACGACGACGACGACGACGACGACGACGACGACGACGACGAC 412
QY 429 GGATCGGCTTACCGCTACAACTACATCGCAAGTCAACACTGTCAAAAAGCTC 483
DB 413 CAACGACAAACGACGACGACGACGACGACGACGACGACGACGACGACGAC 467

RESULT 5
CB640993
LOCUS
DEFINITION
OSJNEal7F21.f OSJNEA Oryza sativa (japonica cultivar-group) CDNA clone OSJNEal7F21 5', mRNA sequence.
ACCESSION
CB640993

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VERSION CB640993.1 GI:29635984
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 591)
AUTHORS Jantaauriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
TITLE Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
JOURNAL Plant Physiol. 138 (1), 105-115 (2005)
PUBMED 1588683
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: atc agc ggc cgc gat cc
BACKWARD: aat taa ccc tca cta aag gg
Plate: 17 row: F column: 21
Seq primer: atc agc ggc cgc gat cc.
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/mol_type="mRNA"
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/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSUNB"
/notes="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 6 hrs after inoculation with Rice Blast (Che
86061)"
ORIGIN
Query Match 10.2%; Score 53.6; DB 6; Length 591;
Best Local Similarity 44.5%; Pred. No. 0.00077;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;
Qy 41 CGCGCGCGCACTGGCGGAAGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACAG 100
Db 36 CAGCAGCGGCATGGAGGGATACGACCGGAGTTCTACCACTTCCAGCAGCTGGCGC 95
Qy 101 CAAAAGCTCAAGCTCTTAGGTTCTGCAAGAGCTTCAGCCCGCATCTCCGCAAGCT 160
Db 96 TGCAGACGGCGAGCTTCTCCGGCTCTCCCTCGCGACTTCCATCTGGTCTCTCCCTCG 155
Qy 161 ACCGCATCAAGCTCCGCTTCGGCTGCGATTCACGCGGTACAAAACCTATAAAGCC 220
Db 156 ACCGCGCAACGAGCGCGCTTCGACGGCGAGTACCACTTCTCTCCCTCCCG 215
Qy 221 CATCCACGATTTCAAACTTTACAGCATCGCGGCTCGCCATTTAGACTTCGACACCC 280
Db 216 CCAAGAGCCCATCGCCAACTCAACGGCTCGCGGAACTGGATGGCCGGGCTCA 275
Qy 281 AATCGCCGTCAAACCGTATCTCGCGCGCGCTTTGAGCTTCAACCGCGCTTCGCTGACT 340
Db 276 TCGGCTCGGCAAGCTTCGCTTCGGCGCCACCAAGCGCGAGCTTACAAAGCGTCAACC 335
Qy 341 TGGGCGCAGCAGCTTCAGCCAAACCTTCATCGGCTCGGCTGATTTAGCGGGCGTAA 400
Db 336 TCCCGCTCGAACAACAACAACAACAAGTCTTACGGCGGCGCGCCCAAGATCAACAACA 395
Qy 401 GCTATGCGGTTACCCCGAATGTGATTTGGATGGCGGCTACCGCTACAACTACATCGGCA 460
396 ACAACGTCAACGCTTCGGGTTCAACAAGATGGGGGTTACAACAACGACGACGCGC 455
461 AAGTCACACTGTCAAAAAGCTCGGTCGGCGAGACTGTTCGGTGGGGTGGCGTC 516
456 GCGCAACTAGCGCGGACACGCGGCGGCGAGCTGAAGAGCTACTTTCAACAAGTCGGTC 511
RESULT 6
CV152413 665 bp mRNA linear EST 08-SEP-2004
LOCUS LS245-S.SEQ Cold stressed rice cDNA library Oryza sativa (japonica
cultivar-group) cDNA, mRNA sequence.
ACCESSION CV152413
VERSION CV152413.1 GI:51946072
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 665)
AUTHORS Lee,J.-S.
TITLE Isolation and chromosomal mapping of the rice clones differentially
induced under abiotic stress conditions
JOURNAL Unpublished (2004)
COMMENT Contact: Lee Jung-Sook
Bioinformatics Team
National Institute of Agricultural Biotechnology, Rural Development
Administration
225 Seodundon, Suwon, 441-707, Korea
Tel: 82 31 299 1663
Fax: 82 31 299 1722
Email: junglee@da.go.kr.
FEATURES
source
1..665
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Ilpumbyeol"
/db_xref="taxon:39947"
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/clone_lib="Cold stressed rice cDNA library"
/notes="Vector: pBluescript SK+; Cold treatment by placing
at 40C for 16 hour after growth on MS medium for one week"
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Query Match 10.2%; Score 53.6; DB 7; Length 665;
Best Local Similarity 44.5%; Pred. No. 0.00078;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;
Qy 41 CGCGCGCGCACTGGCGGAAGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACAG 100
Db 46 CAGCAGCGGCATGGAGGGATACGACCGGAGTTCTACCACTTCCAGCAGCTGGCGC 105
Qy 101 CAAAAGCTCAAGCTCTTAGGTTCTGCAAGAGCTTCAGCCCGCATCTCCGCAAGCT 160
Db 106 TGCAGAGCGGAGCTTCTCGGCTCTCCCTCGCGACTTCATCTGGTCTCTCCCTCG 165
Qy 161 ACCGCATCAACGACTTCGGCTTCGGCTGCGATTCACGCGGTACAAAACCTATAAAGCC 220
Db 166 ACCGCGCAACGAGCGCGCTTCGACGGCGAGTACCACTTCTCTCCCTCCCG 225
Qy 221 CATCCACGATTTCAAACTTTACAGCATCGCGGCTCGCCATTTAGACTTCGACACCC 280
Db 226 CCAAGAACGCGCATCGCCAACTCAACGGCTCGCGGAAACCTGGATGGCCGGGCTCA 285
Qy 281 AATCGCCGTCAAACCGTATCTCGCGCGCGCTTTGAGCTTCAACCGCGCTTCGCTGACT 340
Db 286 TCGGCTCGGCAAGCTTCGCTTCGGCGCCACCAAGCGCGAGCTTACAAAGCGTCAACC 345
Qy 341 TGGGCGCAGCAGCTTCAGCCAAACCTTCATCGGCTTCGGCTGATTTAGCGGGCGTAA 400
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Db      346  TCCCGTCGACAAACAACAACAACAGTCTACGGCGGCCGCCCAAGATCAACAACA 405
Qy      401  GCTATGCCGTTTACCCCGAATTCGATTTGGATGCCGCTACCGCTACAACTACATCGGCA 460
Db      406  ACAAGTCAACGCCCTTCGGGTTTCAACAAGATGGGGGTTTACAACAACAGCAGCAGCGCG 465
Qy      461  AAGTCAACACTGTCTAAAAACGTCGCTTCGGGGGAACCTGCTCGTGGCGTGCGCGTC 516
Db      466  GCGGCAACTACGGCGCAACGCGCGAGCTGCTTCAACAAGTGGGTC 521

RESULT 7
CB653730
LOCUS      OSJNEC05A17.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
DEFINITION clone OSJNEC05A17 5', mRNA sequence.
ACCESSION CB653730
VERSION    CB653730.1 GI:29657455
KEYWORDS   EST.
ORGANISM   Oryza sativa (japonica cultivar-group)
SOURCE     Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
            Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
            Soderlund,C. and Wang,G.L.
            Large-scale identification of expressed sequence tags involved in
            rice and rice blast fungus interaction
            Plant Physiol. 138 (1), 105-115 (2005)
            1588683
COMMENT     Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: rwing@genome.arizona.edu
            PCR Primers
            FORWARD: gta aaa cga cgg cca gtc
            BACKWARD: gga aac agc tat gac cat g
            Plate: 05 row: A column: 17
            Seq primer: gta aaa cga cgg cca gtc.
            Location/Qualifiers
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            /mol_type="mRNA"
            /db_xref="taxon:39947"
            /clone="OSJNEC05A17"
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            /dev_stage="3 week"
            /lab_host="DH10B"
            /clone_lib="OSJNEC"
            /note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
            XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

Query Match      10.2%; Score 53.6; DB 6; Length 698;
Best Local Similarity 44.5%; Pred. No. 0.00079;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

Qy      41  CGGCGCGCATCGCGGAAGCGCATCGGGTTTTTGTCTCAAGCCGATGCGCGCAGG 100
Db      47  CAGCAGCGGCATGAGGAGATACGACCGCGAGTTCTACAGTCCCGCGCAGCAGTGGCGC 106
Qy      101  CAAGAAGCTCTAGCTCTTTAGTCTCTGCCAAGGCTTCAGCCGCGCATCTCGCAGGCT 160
Db      107  TGCAGAGCGGAGCTTCTTCGCGCCCTCTCTTCGCGGACTTCAATCTGTCCTCCCTCG 166
Qy      161  ACCGCATCAACGACCTCGCTTCGCGCTCGATTACACGCGCTACAAAACCTATAAGCCC 220

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Db      167  ACCGCGCAACGAGCGCGCCTTCGACGCGGAGTACCACTTCTCTCCCTCCCGCG 226
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Db      227  CCAAGAACGCCATCGCAACATCAACGCGTTCGCGGAAACCTGGATGCGCGGCGCTCA 286
Qy      281  AATCGCGCTCAAAACGCTATCTCGCGCGCGCTTGAAGCTCAACCGCGCTTCGCTGACT 340
Db      287  TCGGCTCGGCAAGCTCGCCTTCGCGGCCACCAAGCGCGCTTACAACAGCGTCAACC 346
Qy      341  TGGGCGGCGAGCAGCTTCAGCCAAACCTCATCGGCTCGGCTATTGAGCGCGTAA 400
Db      347  TCCCGCTCGACAACAACAACAACAAGTCTTACGCGGCGGCCGCCCAAGATCAACAACA 406
Qy      401  GCTATGCCGTTTACCCCGAATTCGATTTGGATGCCGCTACCGCTACAACTACATCGGCA 460
Db      407  ACAAGCTCAACGCCCTTCGGGTTCAACAGATGGGGGTTACAACAACAGCAGCAGCGCG 466
Qy      461  AAGTCAACACTGTCTAAAAACGTCGCTTCGGGGGAACCTGCTCGTGGCGTGCGCGTC 516
Db      467  GCGGCAACTACGGCGCAACGCGCGAGCTGCTTCAACAAGTGGGTC 522

RESULT 8
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LOCUS      725 bp mRNA linear EST 09-APR-2003
DEFINITION clone OSJNE14E24 5', mRNA sequence.
ACCESSION CB677411
VERSION    CB677411.1 GI:29681136
KEYWORDS   EST.
ORGANISM   Oryza sativa (japonica cultivar-group)
SOURCE     Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
            1 (bases 1 to 725)
            Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
            Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
            Soderlund,C. and Wang,G.L.
            Large-scale identification of expressed sequence tags involved in
            rice and rice blast fungus interaction
            Plant Physiol. 138 (1), 105-115 (2005)
            1588683
COMMENT     Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: rwing@genome.arizona.edu
            PCR Primers
            FORWARD: gta aaa cga cgg cca gtc
            BACKWARD: gga aac agc tat gac cat g
            Plate: 14 row: B column: 24
            Seq primer: gta aaa cga cgg cca gtc.
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            /clone_lib="OSJNE"
            /note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
            XhoI; 24 hrs after inoculation with Rice Blast (70-15)"

FEATURES
            source

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ORIGIN

Query Match 10.2%; Score 53.6; DB 6; Length 725;
Best Local Similarity 44.5%; Pred. No. 0.00079;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

Qy 41 CGGCGCGGCACTGGCGAAGCGCATCGCGCTTTTACGTCAAGCCGATCGCGCACAG 100
Db 22 CAGCAGCGGCCATGGAGGGATACGACCGCGAGTTCTACCAAGTTTCAGCGACAGCTGCGGC 81

Qy 101 CAAAGCGCTCAAGCTCTTTAGTCTTGCCAAAGGCTTCAGCGCGCATCTCCGCAAGCT 160
Db 82 TGCAGAGCGGAGCTTCTCGGCGCTCTCCCTCGGGGACTCCATCTGGTCTCTCCGCTCG 141

Qy 161 ACCGATCAACGACCTCGCGTTCGCGCTGCGATACAGCGCTTACAAAACATATAAGGCC 220
Db 142 ACCGCGCAACGAGCGCGCTTCGACGCGGAGTACCACTTCTCTCCCTCCCGCTCCCG 201

Qy 221 CATCCACGATTTCAAATTTACAGCATCGGCGGCTCGGCTTACGATTCGACACCC 280
Db 202 CCAAGACGCCATCGCCCAACATCAACGCGCTCGCGGAACCTGGATGGCCCGGCGCTCA 261

Qy 281 AATGCCGCTCAACCGTATCTCGGCGCGCTTGAGGCTCAACCGCGCTCGCTCGACT 340
Db 262 TCGGCTCGGCAAGCTCGCTTCGGCGCCACCAAGCGCGACGCTACCAAGCGTCAACC 321

Qy 341 TGGCGGCGAGCAGCTTCAGCCAACTCCATCGGCTCGGCTGATTTAGCGGCGGTAA 400
Db 322 TCCCGCTCGACAAACAAACAACTCTAGCGCGCGCGCCCAAGATCAACACA 381

Qy 401 GCTATGCGCTTACCGCGAATGTCGATTTGGATGCGGCTACGCTTACATACATCGGCA 460
Db 382 ACAAGCTCAACGCGCTTCGGGTTCAACAGATGGGGGTTTACAACACAGCAGCAACGCG 441

Qy 461 AAGTCAACACTGTCAAAACGTCGTCGCGCACTGCTCGGCGTGGCGCTC 516
Db 442 GCGGCACTACGCGGCAACGCGCGGACGTGAAGAGCTACTTCAACAGTCGGTTC 497

RESULT 9
CF589226
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CF589226
EST00F06 Subtracted cDNA library of JA/BTH-treated rice leaf
sativa (japonica cultivar-group) cDNA clone JBI93, mRNA sequence.
CF589226
CF589226.1 GI:36355281
EST.

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 741)
Yang, Y.

Subtracted cDNA library of JA/BTH-treated rice leaf
Unpublished (2003)
Contact: Yinong Yang
Plant Pathology Department
University of Arkansas
217 Plant Sci Bldg, Fayetteville, AR 72701, USA
Tel: 501-575-5635
Fax: 501 575 7601
Email: yiyang@uark.edu
Seq primer: T7.

FEATURES
source
1..741
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/dev_stage="16-day-old rice seedling treated by JA/BTH"
/clone_lib="Subtracted cDNA library of JA/BTH-treated rice leaf"

/note="Vector: pGEM-T easy; Rice seedling leaves were pretreated with 0.3 mM cycloheximide (CHX) half an hour before treatment of 0.2 mM jasmonic acid (JA) or 0.4 mM benzoethiadiazole (BTH). Both JA- and BTH-induced mRNAs were equally pooled for subtracted cDNA library construction"

ORIGIN
Query Match 10.2%; Score 53.6; DB 6; Length 741;
Best Local Similarity 44.5%; Pred. No. 0.00079;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

Qy 41 CGGCGCGGCACTGGCGAAGCGCATCGCGCTTTTACGTCAAGCCGATCGCGCACAG 100
Db 59 CAGCAGCGGCCATGGAGGGATACGACCGCGAGTTCTACCAAGTTTCAGCGACAGCTGCGGC 118

Qy 101 CAAAGCGCTCAAGCTCTTTAGTCTTGCCAAAGGCTTCAGCGCGCATCTCCGCAAGCT 160
Db 119 TGCAGAGCGGAGCTTCTCGGCGCTCTCCCTCGGCGACTCCATCTGGTCTCTCCCTCCG 178

Qy 161 ACCGATCAACGACCTCGGCTTCGCGCTCGATTAACGCGCTACAAAACTATAAGGCC 220
Db 179 ACCGCGCAACGAGCGCGCTTCGACGCGGAGTACCACTTCTCTCCCTCCCGCTCCCG 238

Qy 221 CATCCACGATTTCAAATTTTACAGCATCGGCGGCTCGGCTTACGATTCGACACCC 280
Db 239 CCAAGAACGCCATCGCCAAACATCAACGCGCTCGCGGAACCTGGATGGCCCGGCGCTCA 298

Qy 281 AATGCCGCTCAACCGTATCTCGGCGCGGCTTGAGGCTCAACCGCGCTCGCTCGACT 340
Db 299 TCGGCTCGGCAAGCTCGCTTCGGCGCCACCAAGCGCGACCGCTTACAACAGCGTCAACC 358

Qy 341 TGGCGCGCAGCAGCTTCAGCCAACTCCATCGGCGCTCGGCTGATTTAGCGGCGGTAA 400
Db 359 TCCCGCTCGACAAACAAACAACTCTAGCGGCGCGCGCCCAAGATCAACACA 418

Qy 401 GCTATGCGCTTACCGCGAATGTCGATTTGGATGCGGCTACCGCTTACATACATCGGCA 460
Db 419 ACAAGCTCAACGCTTCGGGTTCAACAAAGATGGGGGTTTACAACACAGCAGCAACGCG 478

Qy 461 AAGTCAACACTGTCAAAACGTCGTCGCGCACTGCTCGGCGTGGCGCTC 516
Db 479 GCGGCACTACGCGGCAACGCGCGGACGTGAAGAGCTACTTCAACAGTCGGTTC 534

RESULT 10
CB671800
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

CB671800
OSJNE05117.f OSJNEe Oryza sativa (japonica cultivar-group) cDNA clone OSJNE05117 5', mRNA sequence.
CB671800
CB671800.1 GI:29675525
EST.

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 759)
Jantaseuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G., Stahlberg,B., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A., Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
15888683

Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288

Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 05 row: I column: 17
Seq primer: gta aac cga cgg cca gtc.
Location/Qualifiers
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/mol_type="mRNA"
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/lab_host="DH10B"
/clone_lib="OSJNE"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: XhoI; 24 hrs after inoculation with Rice Blast (70-15)"
ORIGIN
Query Match 10.2%; Score 53.6; DB 6; Length 759;
Best Local Similarity 44.5%; Pred. No. 0.00079;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;
QY 41 CGGCCGCGCACTGCGGAAGCGCATCGGCTTTTACGTCCAAAGCGATGCCGACACG 100
DB 35 CAGCAGCGCCATGAGGAGATACGACCGCGAGTTCTACAGTTTCAGCGACGAGTGGCGC 94
QY 101 CAAAGCTCAAGCTCTTTAGGTTCTGCCAAGGCTTCAGCGCGCATCTCCGAGGCT 160
DB 95 TGCAGACGGCGAGCTTCTCCGCGCTCTCCCTCGCGACTTCCATCTGGTCTCCCTCCG 154
QY 161 ACCGCATCAACGACCTCGCTTCGCGCTGATTTACACGCGCTACAAAACTATAAGGCC 220
DB 155 ACCGCGCAACGAGCGGCTTCGACGGGAGTACACACTTCTCTCCCTCCCTCCG 214
QY 221 CATCCACCGATTTCAAACCTTTACAGCATGGCGCGTCCGCCATTTACGACTTCGACACCC 280
DB 215 CCAAGACGCCATCGCCAACTCAACGGCGTCCCGGAAACCTGATGGCGCGGCTCA 274
QY 281 AATCGCGTCAACCGTATCTCGGCGCGCGTTCGAGCTCAACCGCGCTCCGTCGACT 340
DB 275 TCGGCTCGGCAAGCTCGCTTCGCGCGCCACCAAGCGCGACGCTTACAAACGAGCTCAACC 334
QY 341 TGGCGGCGAGCAGAGCTTCAGCAAACTCCATCGGCTGGCGTATTGACGGCGTAA 400
DB 335 TCCCGTGCACAAACAAACAAACAAAGTCTACGGCGGCGCCGCCAAGATCAACAAC 394
QY 401 GCTATCGCGTTACCCCGAATGTGATTTGGATCGCGCTACCGCTACAACTACATCGGCA 460
DB 395 ACAAGTCAACGCTTCGGGTTCAACAGATGGGGGTTACAAACAGCAGCAGCGG 454
QY 461 AAGTCAACACTGTCAAAAAGCTCGTTCGGGGAAGTCTCGCGCGGTGGCGTC 516
DB 455 GCGGCAACTACGCGGCAACGCGCGAGGTGAAGAGCTACTTTCAACAAGTCGCTC 510
RESULT 11
CB677339
LOCUS
DEFINITION
clone OSJNE14C19 5', mRNA sequence.
ACCESSION
CB677339
VERSION
CB677339.1 GI:29681064
KEYWORDS
EST.
ORIGIN
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 762)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
1588683
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 14 row: C column: 19
Seq primer: gta aac cga cgg cca gtc.
Location/Qualifiers
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/clone_lib="OSJNE"
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ORIGIN
Query Match 10.2%; Score 53.6; DB 6; Length 762;
Best Local Similarity 44.5%; Pred. No. 0.00079;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;
QY 41 CGGCCGCGCACTGCGGAAGCGCATCGGCTTTTACGTCCAAAGCGATGCCGACACG 100
DB 33 CAGCAGCGCCATGAGGAGATACGACCGCGAGTTCTACAGTTTCAGCGACGAGTGGCGC 92
QY 101 CAAAGCTCAAGCTCTTTAGGTTCTGCCAAGGCTTCAGCGCGCATCTCCGAGGCT 160
DB 93 TGCAGACGGCGAGCTTCTCCGCGCTCTCCCTCGCGACTTCCATCTGGTCTCCCTCCG 152
QY 161 ACCGCATCAACGACCTCGCTTCGCGCTGATTTACAGCGCTACAAAACTATAAGGCC 220
DB 153 ACCGCGCAACGAGCGGCTTCGACGGGAGTACCACTTCTCTCCCTCCCTCCG 212
QY 221 CATCCACCGATTTCAAACCTTTACAGCATCGCGCGTTCGCCATTTACGACTTCGACACCC 280
DB 213 CCAAGACGCCATCGCCAACTCAACGGCGTCCCGGAAACCTGATGGCGCGGCTCA 272
QY 281 AATCGCGTCAACCGTATCTCGGCGCGCGTTCGAGCTCAACCGCGCTCCGTCGACT 340
DB 273 TCGGCTCGGCAAGCTCGCTTCGCGCGCCACCAAGCGCGCTTACAAACGAGCTCAACC 332
QY 341 TGGCGGCGAGCAGAGCTTCAGCCAACTCCATCGGCTGGCGTATTGACGGCGTAA 400
DB 333 TCCCGTGCACAAACAAACAAACAAAGTCTTACGGCGGCGCCGCCAAGATCAACAAC 392
QY 401 GCTATCGCGTTACCCCGAATGTGATTTGGATCGCGCTACCGCTACAACTACATCGGCA 460
DB 393 ACAAGTCAACGCTTCGGGTTCAACAAGATGGGGGTTACAAACAGCAGCAGCGG 452
QY 461 AAGTCAACACTGTCAAAAAGCTTCGCTTCGGCGGAAGTCTCGCTCGCGGTGGCGTC 516
DB 453 GCGGCAACTACGCGGCAACGCGCGAGCTGAAGAGCTACTTTCAACAAGTCGCTC 508
RESULT 12
CB677062

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LOCUS      CB677062              775 bp      mRNA      linear      EST 09-APR-2003
DEFINITION OSJNEB13K18.f OSJNEB Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEB13K18 5', mRNA sequence.
ACCESSION  CB677062
VERSION     CB677062.1   GI:29680787
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzae; Oryza.
REFERENCE  1 (bases 1 to 775)
AUTHORS   Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
            Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
            Soderlund,C. and Wang,G.L.
TITLE     Large-scale identification of expressed sequence tags involved in
            rice and rice blast fungus interaction
JOURNAL   Plant Physiol. 138 (1), 105-115 (2005)
PUBMED    15888683
COMMENT   Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: rwing@genome.arizona.edu
PCR PRIMERs
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 13 row: K column: 18
Seq primer: gta aaa cga cgg cca gtc.

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/dev_stage="3 week"
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/clone_lib="OSJNEB"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (70-15)"

ORIGIN
Query Match      10.2%; Score 53.6; DB 6; Length 775;
Best Local Similarity 44.5%; Pred. No. 0.0008;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

Qy 41 CGGCGCGCACTGGCGGAGGGCGCATCCGGCTTTAGCTCCAGCCGATCGGCACAG 100
Db 36 CAGCAGCGGCATGGAGGGATACGACCGCGAGTCTACAGTTGAGCCAGCGTGGCG 95

Qy 101 CAAAGCCTCAAGCTCTTTAGGTTCTGCAAGGCTTCAGCCGCGCATCTCCGAGGCT 160
Db 96 TGCAGACGGCGAGCTTCTCCGGCTCTCTCCGCGGACTCCATCTGGTCTCCCTCCG 155

Qy 161 ACCGATCAACGACCTCCGCTTGGCGGCGTTCGATACACCGCTTACAAACATATAAGCCC 220
Db 156 ACCGCGCAACGAGCGCGCTTCGACGCGAGTACCACTTCTCTCCCTCCCTCCCGCG 215

Qy 221 CATCCACGATTTCAAACTTTACAGCATCGGGGCTCGCCATTTACGATTCGCACACC 280
Db 216 CAAAGACCGCATCGCCAACTCAACAGCGGCTCGCCGAAACCTGATGGCCCGGCGCTCA 275

Qy 281 AATCGCCCGTCAAAACCGTATCTCGGCGCGCTTGGAGCTCAACCGCGCTCCGTCGACT 340
Db 276 TCGGCTCGGCNAGCTTCGCTTCGGGCGCACCAAGGCCGACGGCTACAAAGCGTCAACC 335

Qy 341 TGGGCGGAGGACAGCTTTCAGCCAAACCTCCATCGGCTCGGGGTATTTAGCGGGGTAA 400

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Db 336 TCCCCGTCGACAAACAACAACAACAAAGTCTTACGGGGGGCGCCCAAGATCAACAACA 395
Qy 401 GCTATGCGGTTTACCCCGAATGTTCGATTGGATGCGGCTACCGCTACAACTACATCGGCA 460
Db 396 ACAAGGTCACGCTTCGGGTTCAACAAGATGGGGGTTACAACAACAGCAGCAACGCG 455
Qy 461 AAGTCAACACTGTCAAAAACGTCTCGGCGGAACTGTTCGTCGGGTGGCGGCTC 516
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RESULT 13
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LOCUS      OSJNEC07G20.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEC07G20 5', mRNA sequence.
ACCESSION  CB654692
VERSION     CB654692.1   GI:29658417
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzae; Oryza.
REFERENCE  1 (bases 1 to 778)
AUTHORS   Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
            Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
            Soderlund,C. and Wang,G.L.
TITLE     Large-scale identification of expressed sequence tags involved in
            rice and rice blast fungus interaction
JOURNAL   Plant Physiol. 138 (1), 105-115 (2005)
PUBMED    15888683
COMMENT   Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: rwing@genome.arizona.edu
PCR PRIMERs
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 07 row: G column: 20
Seq primer: gta aaa cga cgg cca gtc.

FEATURES             source
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="OSJNEC07G20"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEC"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN
Query Match      10.2%; Score 53.6; DB 6; Length 778;
Best Local Similarity 44.5%; Pred. No. 0.0008;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

Qy 41 CGGCGCGCACTGGCGGAGGGCGCATCCGGCTTTAGCTCCAGCCGATCGGCACAG 100
Db 48 CAGCAGCGGCATGGAGGGATACGACCGCGAGTCTTACAGTTGAGCCAGCGTGGCG 107

Qy 101 CAAAGCCTCAAGCTCTTTAGGTTCTGCAAGGCTTCAGCCCGCGCATCTCCGAGGCT 160
Db 108 TGCAGACGGCGAGCTTCTCCGGCTCTCTCCGCGGACTCCATCTGGTCTCCCTCCG 167

Qy 161 ACCGATCAACGACCTCCGCTTCGCGCTTCGCGTTCGATTAACGCGCTACAAACATATAAGCCC 220

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Db      168 ACCGCGCAACGACCGCGCTTCAGCGCGAGTACCAACCACTTCTCTCCCTCCCTCCCG 227
Qy      221 CATCCACCGATTTCAAACTTTACAGCATCGCGCGTCCGCAATTTAGCACTTCGACACCC 280
Db      228 CCAAGAGCCATCGCCCAACATCAACCGGTGCGCGGAACCTGATGGCCGCGCTCA 287
Qy      281 AATGCGCGTCAAAACGATATCTCGCGCGCGCTTTGAGCTTCAACCGCGCTTCGCTCGACT 340
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Qy      341 TGGGCGCGAGCAGCTTCAGCCAAACCTCCATCGGCTCGGCTATTTAGCGGCGTAA 400
Db      348 TCCCCGTCGACAAACAAACAAACAGTCTTACGCGCGCGCGCCCAAGATCAACAA 407
Qy      401 GCTATGCGCTTACCCCAATGTCGATTTGATGCGGCTACCGCTTACAACTACATCGGCA 460
Db      408 ACAAGTCAAGCTTCGCGTTCAACAAGATGGGGGTTTACAAACAGCAGCAAGCGG 467
Qy      461 AAGTCAACACTGTCAAAAACGTCGTTCCGCGCAACTGTCTCGGCGTGGCGTC 516
Db      468 GCGCAACTACGCGCGCAACGCGGCGACGTGAAGAGCTACTTCAACAAGTGGTC 523

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RESULT 14
CB665147
LOCUS
DEFINITION
OSJNEd11P07.f OSJNEd Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEd11P07 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
1 (bases 1 to 782)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C., and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
1588683

Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 11 row: F column: 07
Seq primer: gta aac cga cgg cca gtg.

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nipponbare"
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/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEd"
/notes="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 24 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN

Query Match 10.2%; Score 53.6; DB 6; Length 782;
Best Local Similarity 44.5%; Pred. No. 0.0008;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

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Qy      41 CGGCGCGCACCTGGGAGGCGCATCCGGCTTTTACGTCCCAAGCGCGATGCCGACACG 100
Db      38 CAGAGCGGCATGGAGGATACGCGCGAGTTCTACAGTTTACGAGCAGCTCGGCG 97
Qy      101 CAAAAGCCTCAAGCTCTTTAGGTTTGCCTCAAGAGCTTTAGCCCGCGCATTCGCGAGGCT 160
Db      98 TGCAGAGCGGAGCTTCTCCGGCTCTCCCTCGCGACTCCATCTGCTCTCCCTCCG 157
Qy      161 ACCGATCAACGACCTCCGCTTCGCGTTCGATTTACAGCGCTTACAAAATATAAGCCC 220
Db      158 ACCGCGCACGAGCGCGCTTCGAGCGGAGTACCACCACTTCTCTCCCTCCG 217
Qy      221 CATCCACCGATTTCAAACTTTACAGCATCGGCGCTCCGCCATTTACGATTCGACACCC 280
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Qy      281 AATCGCGCTCAAAACGCTATCTCGGCGCGCTTTGAGCTTCAACCGCGCTTCGCTCGACT 340
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Qy      461 AAGTCAACACTGTCAAAAACGTCGCTTCGCGCAACTGTCTCGCGCTCGGCTC 516
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RESULT 15
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LOCUS
DEFINITION
OSJNEd15K14.f OSJNEd Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEd15K14 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
1 (bases 1 to 842)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C., and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
1588683

Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 15 row: K column: 14
Seq primer: gta aac cga cgg cca gtg.

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
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/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEd"
/notes="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 24 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN

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/mol_type="mRNA"
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/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEd"
/notes="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (C9240-1)"
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Query Match      10.2%; Score 53.6; DB 6; Length 842;
Best Local Similarity 44.5%; Pred. No. 0.0008;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

Qy 41 CGGCGCGCGCACTGGCGGAGGGCGCATCCGGCTTTTACGTCCAAAGCGGATGCCGCGACAG 100
Db 42 CAGCAGCGCGCATGGAGGGATACGACCGCGAGTTCTACCAAGTTTCAGCGACAGCTGCGGC 101
Qy 101 CAAAAGCCTCAAGCTCTTTAGGTTCTGCCAAGGCTTCAGCCCGCGCATCTCCGAGGCT 160
Db 102 TGCAGAGCGGAGCTTCTCCGGCTCTCCCTCGCGGACTCCATCTGGTCTCTCCCTCCG 161
Qy 161 ACCGCATCAACGACCTCCGCTTCGCGCTCGATTACACGCGCTACAAAACTATAAAGCCC 220
Db 162 ACCGCGCAACGAGCGGCGCTTCGACGGCGAGTACCACCACTTCTCTCCCTCCCTCCCG 221
Qy 221 CATCCACCGATTTCAAACTTTACAGCATCGCGCGGTCGCGCATTTAGCACTTCGACACCC 280
Db 222 CCAAGAACGCCATCGCCCAACATCAACGCGCTCGCGGAAACCTGGATGGCGCGGCTCA 281
Qy 281 AATCGCCGTCACACCGTATCTCGCGCGGCTTGAGCCTCAACCGCGCTTCGTCGACT 340
Db 282 TCGGCTCCGCAAGCTCGCCTTCGGCGCCACCAAGGCCGACCGCTAACAGCGTCAACC 341
Qy 341 TGGCGCGGACGACAGCTTCAGCCAAACCTCCATCGGCTTCGGCTATTGACGGGGTAA 400
Db 342 TCCCGTTCGACACACACAAACAACAAGTCTCTACGGGGGCGCGCCAGATCAACAACA 401
Qy 401 GCTATGCCGTTACCCCGAATGTGATTTGGATGCCGGCTACCGCTACAACTACATCGGCA 460
Db 402 ACAACGTCAACGCTTCGGGTTCAACAAGATGGGGGTTACAACAACAGCAGCAACGGCG 461
Qy 461 AAGTCAACACTGTCAAAAGCTCGTTCCGCGCACTGTCCGTCCGGTGGGGTTC 516
Db 462 GCGCAACTACGGCGCAACGCGCGGACGTGAAGACTTCTTCAACAAGTCGGTC 517
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Search completed: January 12, 2006, 22:10:10
Job time : 3285 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 11, 2006, 15:21:38 ; Search time 115 Seconds
(without alignments)
632.194 Million cell updates/sec

Title: US-10-650-123-2
Perfect score: 868
Sequence: 1 MKKALATLIALPAALAE.....VNTKVRSGELSGVRVKF 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	868	100.0	174	3	US-09-870-759-36
2	868	100.0	174	3	US-09-751-708A-36
3	868	100.0	174	4	US-10-650-123-2
4	868	100.0	174	4	US-10-428-817A-32
5	868	100.0	174	5	US-10-937-758A-36
6	864	99.5	174	4	US-10-320-800-4
7	864	99.5	174	5	US-10-988-943-20
8	825	95.0	174	4	US-10-467-534-90
9	206	23.7	241	5	US-10-988-943-16
10	122.5	14.1	94	5	US-10-795-159-735
11	103.5	11.9	350	5	US-10-946-647-1377
12	103	11.9	228	4	US-10-282-122A-69437
13	101	11.6	21	4	US-10-082-014-124
14	101	11.6	21	4	US-10-372-076-125
15	101	11.6	21	4	US-10-732-862A-139
16	101	11.6	21	4	US-10-677-074-125
17	99.5	11.5	350	4	US-10-282-122A-77105
18	99	11.4	210	4	US-10-282-122A-55523
19	98.5	11.3	350	5	US-10-946-647-1389
20	98.5	11.3	350	5	US-10-946-647-1395
21	98.5	11.3	350	5	US-10-946-647-1404
22	97	11.2	21	4	US-10-082-014-123
23	97	11.2	21	4	US-10-372-076-124
24	97	11.2	21	4	US-10-732-862A-138
25	97	11.2	21	4	US-10-677-074-124
26	97	11.2	353	4	US-10-467-421-21
27	94.5	10.9	212	3	US-09-815-242-10149

ALIGNMENTS

RESULT 1
US-09-870-759-36
; Sequence 36, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 36
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-870-759-36

Query Match	100.0%	Score 868;	DB 3;	Length 174;
Best Local Similarity	100.0%	Pred. No. 4.1e-85;		
Matches 174;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR	60	
Db	1	MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR	60	
Qy	61	FAVDYTRYKNYKAPSTDPKLYSIGASALYDFTQSPVKPYLGCARLSLRASVDLGGSDSF	120	
Db	61	FAVDYTRYKNYKAPSTDPKLYSIGASALYDFTQSPVKPYLGCARLSLRASVDLGGSDSF	120	
Qy	121	SQTSIGLGLVAGSVAVTFPNVDLDAGYRNYIGKVTYKVRSGELSGVGRVKF	174	
Db	121	SQTSIGLGLVAGSVAVTFPNVDLDAGYRNYIGKVTYKVRSGELSGVGRVKF	174	

RESULT 2
US-09-751-708A-36
; Sequence 36, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-751-708A-36

Query Match          100.0%; Score 868; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.1e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120

Qy 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174
Db 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174

RESULT 3
US-10-650-123-2
; Sequence 2, Application US/10650123
; Publication No. US20040132652A1
; GENERAL INFORMATION:
; APPLICANT: Shire BioChem Inc.
; TITLE OF INVENTION: PHARMACEUTICAL LIPOSOMAL COMPOSITIONS CONTAINING N.MENINGITIDIS D
; FILE REFERENCE: 74872-94
; CURRENT APPLICATION NUMBER: US/10/650,123
; PRIOR FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US 60/406,980
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 174
; TYPE: PRT
; ORGANISM: N. meningitidis strain 608B
US-10-650-123-2

Query Match          100.0%; Score 868; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.1e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120

Qy 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174
Db 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174

RESULT 4
US-10-428-817A-32
; Sequence 32, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
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; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-428-817A-32

Query Match          100.0%; Score 868; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.1e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120

Qy 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174
Db 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174

RESULT 5
US-10-937-758A-36
; Sequence 36, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-937-758A-36

Query Match          100.0%; Score 868; DB 5; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.1e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120

Qy 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174
Db 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174
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RESULT 6
US-10-320-800-4
; Sequence 4, Application US/10320800
; Publication No. US20030215469A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, ANDREW
; APPLICANT: GORRINGE, ANDREW
; APPLICANT: HUDSON, MICHAEL
; APPLICANT: REDDIN, KAREN
; TITLE OF INVENTION: MULTICOMPONENT MENINGOCOCCAL VACCINE
; FILE REFERENCE: 1581.0790001
; CURRENT APPLICATION NUMBER: US/10/320,800
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: PCT/GB99/03626
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-320-800-4
Query Match 99.5%; Score 864; DB 4; Length 174;
Best Local Similarity 99.4%; Pred. No. 1.1e-84;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRSYDLGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRSYDLGSDSF 120
QY 121 SQTSLGLGLTGVSVAVTPNVDLDAGYRNYIGKVTNKVNRSGELSGVGRVKF 174
DB 121 SQTSLGLGLTGVSVAVTPNVDLDAGYRNYIGKVTNKVNRSGELSGVGRVKF 174
RESULT 7
US-10-988-943-20
; Sequence 20, Application US/10988943
; Publication No. US20050176085A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
; TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR THE
; TITLE OF INVENTION: IDENTIFICATION AND QUANTITATIVE ANALYSIS OF PROTEINS IN
; FILE REFERENCE: Proteomics CU2003-269
; CURRENT APPLICATION NUMBER: US/10/988,943
; CURRENT FILING DATE: 2004-11-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Neisseria meningitidis (group B)
US-10-988-943-20
Query Match 99.5%; Score 864; DB 5; Length 174;
Best Local Similarity 99.4%; Pred. No. 1.1e-84;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRSYDLGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRSYDLGSDSF 120

QY 121 SQTSLGLGLTGVSVAVTPNVDLDAGYRNYIGKVTNKVNRSGELSGVGRVKF 174
DB 121 SQTSLGLGLTGVSVAVTPNVDLDAGYRNYIGKVTNKVNRSGELSGVGRVKF 174
RESULT 8
US-10-467-534-90
; Sequence 90, Application US/10467534
; Publication No. US20040131625A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Verlant, Vincent Georges Christian Louis
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45261
; CURRENT APPLICATION NUMBER: US/10/467,534
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: PCT/EP02/01356
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103169.9
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-534-90
Query Match 95.0%; Score 825; DB 4; Length 174;
Best Local Similarity 94.3%; Pred. No. 1.8e-80;
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRSYDLGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRSYDLGSDSF 120
QY 121 SQTSLGLGLTGVSVAVTPNVDLDAGYRNYIGKVTNKVNRSGELSGVGRVKF 174
DB 121 SQTSLGLGLTGVSVAVTPNVDLDAGYRNYIGKVTNKVNRSGELSGVGRVKF 174
RESULT 9
US-10-988-943-16
; Sequence 16, Application US/10988943
; Publication No. US20050176085A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
; TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR THE
; TITLE OF INVENTION: IDENTIFICATION AND QUANTITATIVE ANALYSIS OF PROTEINS IN
; FILE REFERENCE: Proteomics CU2003-269
; CURRENT APPLICATION NUMBER: US/10/988,943
; CURRENT FILING DATE: 2004-11-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Neisseria meningitidis (group B)
US-10-988-943-16
Query Match 23.7%; Score 206; DB 5; Length 241;
Best Local Similarity 26.4%; Pred. No. 1.4e-13;
Matches 62; Conservative 30; Mismatches 59; Indels 84; Gaps 7;
QY 23 SGFYVQADAAHA-----KASSLSG-----AKGFSRISAGYRINDLRPA 62

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Db      8 SPYTVQADLAYAABERITHDYPKATCANNTSTVSYFRNIRAHSHIPRVSVGYDFGWRRIA 67
Qy      63 VDYTRYKNY-----KAPSTDPKLYSIGASAIYDF--- 91
Db      68 ADYASYRKWNKKYSVNTKELQKNSSGIWQELKTENQENGTFHAASSGLSALIYDFKLN 127
Qy      92 DTQSPVKPYLGLARLSINRA-----SVDLGGSDSPSQ----- 122
Db      128 DKPDKFKYIGARVAYGHVKQVHSVRKEITTTTSPPAQGATVPQKIVQGTNKPAYHES 187
Qy      123 ---TSIGLGVLTGVSAYVTPNVDLDAGRYNYIKVNTVKNVRSGELSVGVVRKF 174
Db      188 NSISSLGLGVAGVGFDTPKLTLDGYRYHNGRLENTR-FKTHEVSLGRMYHF 241

RESULT 10
US-10-795-159-735
; Sequence 735, Application US/10795159
; Publication No. US20050221439A1
; GENERAL INFORMATION:
; APPLICANT: BAKALETZ et al.
; TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPEABLE H. INFLUENZAE
; FILE REFERENCE: 28335/38615A
; CURRENT APPLICATION NUMBER: US/10/795,159
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 60/453,134
; PRIOR FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 771
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 735
; LENGTH: 94
; TYPE: PRT
; ORGANISM: H. influenzae
US-10-795-159-735

Query Match 14.1%; Score 122.5; DB 5; Length 94;
Best Local Similarity 33.3%; Pred. No. 3.8e-05;
Matches 30; Conservative 15; Mismatches 36; Indels 9; Gaps 2;

Qy      93 TQSPVKPYLGLARLSINRAVDLGG-----SDSFSQTSIGLGVLTGVSAYVTPNVDLD 144
Db      6 TSGYTKDEFKTLTKLTPKTNMPPIGDVKADQBTSGRSIKRIGFGFIGGIDYDITENITLD 65
Qy      145 AGRYNYIKVNTVKNVRSGELSVGVVRKF 174
Db      66 LDYRYNDWGRLENVR-FKTHEASFGVRYRP 94

RESULT 11
US-10-946-647-1377
; Sequence 1377, Application US/109466647
; Publication No. US20050186217A1
; GENERAL INFORMATION:
; APPLICANT: EMERY, DARYLL A.
; APPLICANT: STRAUB, DARREN E.
; APPLICANT: WONDERLING, LAURA
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
; FILE REFERENCE: 293.00340101
; CURRENT APPLICATION NUMBER: US/10/946,647
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: 60/504,119
; PRIOR FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 1448
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1377
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Salmonella enterica
US-10-946-647-1377

Query Match 11.9%; Score 103.5; DB 5; Length 350;
Best Local Similarity 24.3%; Pred. No. 0.026;
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Matches 50; Conservative 28; Mismatches 85; Indels 43; Gaps 8;
Qy      1 MKK-ALATLIALAPAAALAEAGSGFYVQADAAHAHAKASSIGSAGFSPRISAGYRIND- 58
Db      1 MKKTAIAIAVALA-----GFATVAQAAPKDNWTYAGAKLGSQYHDTGFIHNDG 49
Qy      59 -----LRPAVDYTRYKNYKAPSTD--PKLYSIGASAIYDFDTQ 94
Db      50 PTHENQLGAGAFGGYQNPVYVPEMGYDMLGRMPYKGDNTNGAYKAQGVQLTAKLGYPIIT 109
Qy      95 SPVKPY--LGARL--SLNRASVDLGGSDSPSQTSIGLGVLTGVSAYVTPNVDLDAGYR- 149
Db      110 DDLDDVYTRLGGVMWRADTKSNVPGGASTKHDDTGTGVSVPFAGGIBYAITPEIATRLQYWT 169
Qy      150 NYICKVNTV--KNVRSGELSVGVVRKF 174
Db      170 NNIGDANTIGTRPDNGLLSVGVSRYF 195

RESULT 12
US-10-282-122A-69437
; Sequence 69437, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69437
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Pseudomonas syringae
US-10-282-122A-69437

Query Match 11.9%; Score 103; DB 4; Length 228;
Best Local Similarity 25.8%; Pred. No. 0.016;
Matches 54; Conservative 23; Mismatches 90; Indels 42; Gaps 7;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 11, 2006, 15:22:23 ; Search time 29 Seconds
(without alignments)
56.725 Million cell updates/sec

Title: US-10-650-123-2

Perfect score: 868

Sequence: 1 MKKALATLIALPALPAALAE.....VNTKVRSGELSGVVRVKF 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_New.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pap.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
- 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
- 5: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pap.*
- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pap.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	100.0	174	6	US-10-984-376-7
2	862	99.3	174	6	US-10-984-376-8
3	852	98.2	174	6	US-10-984-376-10
4	852	98.2	174	6	US-10-984-376-11
5	849	97.8	174	6	US-10-984-376-9
6	846	97.5	174	6	US-10-984-376-12
7	825	95.0	174	7	US-11-103-957-90
8	809.5	93.3	175	6	US-10-467-657-2512
9	805	92.7	174	6	US-10-984-376-13
10	785.5	90.5	173	6	US-10-984-376-14
11	785.5	90.5	173	6	US-10-984-376-13
12	218.5	25.2	229	6	US-10-467-657-6238
13	218.5	25.2	229	6	US-10-467-657-6238
14	214	24.7	281	6	US-10-467-657-8006
15	212	24.4	278	6	US-10-467-657-8006
16	210	24.2	265	6	US-10-467-657-1778
17	208	24.0	161	7	US-11-052-554A-86
18	207.5	23.9	186	6	US-10-467-657-7854
19	206	23.7	278	6	US-10-467-657-7386
20	204.5	23.6	229	6	US-10-467-657-1754
21	194.5	22.4	227	6	US-10-467-657-54
22	194.5	22.4	227	6	US-10-467-657-830
23	178	20.5	189	6	US-10-467-657-3184
24	94.5	10.9	212	7	US-11-052-554A-198
25	88.5	10.2	703	7	US-11-052-554A-97

26	87.5	10.1	792	7	US-11-103-957-25	Sequence 25, Appl
27	81.5	9.4	351	7	US-11-052-554A-203	Sequence 203, Appl
28	79	9.1	16	6	US-10-984-376-17	Sequence 17, Appl
29	77	8.9	15	6	US-10-984-376-18	Sequence 18, Appl
30	74	8.5	291	6	US-10-821-234-1560	Sequence 1560, Ap
31	74	8.5	690	7	US-11-052-554A-99	Sequence 99, Appl
32	73.5	8.5	180	7	US-11-052-554A-343	Sequence 343, Appl
33	72.5	8.4	338	7	US-11-016-564-4	Sequence 4, Appl
34	72.5	8.4	344	7	US-11-096-850-1	Sequence 1, Appl
35	72	8.3	222	7	US-11-052-554A-338	Sequence 338, Appl
36	71.5	8.2	955	7	US-11-052-554A-179	Sequence 179, Appl
37	71	8.2	669	6	US-10-878-556A-87	Sequence 87, Appl
38	71	8.2	721	7	US-11-060-920-5	Sequence 5, Appl
39	70.5	8.1	199	7	US-11-052-554A-62	Sequence 62, Appl
40	70.5	8.1	199	7	US-11-052-554A-63	Sequence 63, Appl
41	70.5	8.1	199	7	US-11-052-554A-64	Sequence 64, Appl
42	69.5	8.0	337	7	US-11-096-850-5	Sequence 5, Appl
43	69.5	8.0	528	6	US-10-858-730-88	Sequence 88, Appl
44	69.5	8.0	1565	6	US-10-467-657-2704	Sequence 2704, Ap
45	69.5	8.0	3157	7	US-11-052-554A-142	Sequence 142, Appl

ALIGNMENTS

RESULT 1
US-10-984-376-7
; Sequence 7, Application US/10984376
; Publication No. US20050244436A1
; GENERAL INFORMATION:
; APPLICANT: GIULIANI, Marzia Monica
; APPLICANT: PIZZA, Mariagrazia
; APPLICANT: RAPPUOLI, Rino
; TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS
; FILE REFERENCE: 2300-1609.20
; CURRENT APPLICATION NUMBER: US/10/984,376
; CURRENT FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: 09/979,263
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: PCT/IB00/00828
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: GB 911692.3
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: GB 9919705.5
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: GB 0005730.7
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 7
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nepa
US-10-984-376-7

Query Match						100.0%; Score 868; DB 6; Length 174;
Best Local Similarity						100.0%; Pred. No. 5.2e-79;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	1	MKKALATLIALPALPAALAE	CGFYVQADAAHAKASSLSGAKGFS	PRISAGYRINDLR	60	
Db	1	MKKALATLIALPALPAALAE	CGFYVQADAAHAKASSLSGAKGFS	PRISAGYRINDLR	60	
Qy	61	FADVTRYKNTKASTDFKLS	IGASAIYDFTQSPVKPYL	GARLSLNRSVDL	CGSDSF 120	
Db	61	FADVTRYKNTKASTDFKLS	IGASAIYDFTQSPVKPYL	GARLSLNRSVDL	CGSDSF 120	
Qy	121	SQTSIGLVGLGVSVAVTP	PNVDLDAGYRNYIGKNT	VKNVRSBELSV	GVVRVKF 174	
Db	121	SQTSIGLVGLGVSVAVTP	PNVDLDAGYRNYIGKNT	VKNVRSBELSV	GVVRVKF 174	

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RESULT 2
US-10-984-376-8
; Sequence 8, Application US/10984376
; Publication No. US2005024436A1
; GENERAL INFORMATION:
; APPLICANT: GIULIANI, Marzia Monica
; APPLICANT: PIZZA, Mariagrazia
; APPLICANT: RAPPUOLI, Rino
; TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS
; FILE REFERENCE: 2300-1609.20
; CURRENT APPLICATION NUMBER: US/10/984.376
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: 09/979,263
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: PCT/IB00/00828
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: GB 9911692.3
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: GB 9919705.5
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: GB 0005730.7
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nsnpa
US-10-984-376-8

Query Match      99.3%; Score 862; DB 6; Length 174;
Best Local Similarity 99.4%; Pred. No. 2e-78;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db      1  MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy      61  FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
Db      61  FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120

Qy      121  SOTSIGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 174
Db      121  SOTSIGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 174

RESULT 3
US-10-984-376-10
; Sequence 10, Application US/10984376
; Publication No. US2005024436A1
; GENERAL INFORMATION:
; APPLICANT: GIULIANI, Marzia Monica
; APPLICANT: PIZZA, Mariagrazia
; APPLICANT: RAPPUOLI, Rino
; TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS
; FILE REFERENCE: 2300-1609.20
; CURRENT APPLICATION NUMBER: US/10/984.376
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: 09/979,263
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: PCT/IB00/00828
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: GB 9911692.3
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: GB 9919705.5
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: GB 0005730.7
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nsnpa
US-10-984-376-11

Query Match      98.2%; Score 852; DB 6; Length 174;
Best Local Similarity 98.3%; Pred. No. 2e-77;
Matches 171; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1  MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db      1  MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy      61  FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
Db      61  FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120

Qy      121  SOTSIGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 174
Db      121  SOTSIGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 174

RESULT 4
US-10-984-376-11
; Sequence 11, Application US/10984376
; Publication No. US2005024436A1
; GENERAL INFORMATION:
; APPLICANT: GIULIANI, Marzia Monica
; APPLICANT: PIZZA, Mariagrazia
; APPLICANT: RAPPUOLI, Rino
; TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS
; FILE REFERENCE: 2300-1609.20
; CURRENT APPLICATION NUMBER: US/10/984.376
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: 09/979,263
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: PCT/IB00/00828
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: GB 9911692.3
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: GB 9919705.5
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: GB 0005730.7
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nsnpa
US-10-984-376-11

Query Match      98.2%; Score 852; DB 6; Length 174;
Best Local Similarity 98.3%; Pred. No. 2e-77;
Matches 171; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1  MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db      1  MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy      61  FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
Db      61  FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120

Qy      121  SOTSIGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 174
Db      121  SOTSIGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 174
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; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NspA
; US-10-984-376-12

Query Match          97.5%; Score 846; DB 6; Length 174;
Best Local Similarity 97.7%; Pred. No. 7.8e-77;
Matches 170; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALAAEGAGSGFFVQDAADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALAAEGAGSGFFVQDAADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSINRASVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSINRASVDLGGSDSF 120

QY 121 SQTISGLGLVGTGSYAVTPNVLDLADAGRYNYIGKVTXKNVRSGBLSVGVVRVKF 174
Db 121 SQTISGLGLVGTGSYAVTPNVLDLADAGRYNYIGKVTXKNVRSGBLSVGVVRVKF 174

RESULT 7
US-11-103-957-90
; Sequence 90, Application US/11103957
; Publication No. US20050281847A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Verilant, Vincent Georges Christian Louis
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45261
; CURRENT APPLICATION NUMBER: US/11/103,957
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: US/10/467,534
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/EP02/01356
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103169.9
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-11-103-957-90

Query Match          95.0%; Score 825; DB 7; Length 174;
Best Local Similarity 94.3%; Pred. No. 9.2e-75;
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALAAEGAGSGFFVQDAADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALAAEGAGSGFFVQDAADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSINRASVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYFGARLSINRASVHLGGSDSF 120

QY 121 SQTISGLGLVGTGSYAVTPNVLDLADAGRYNYIGKVTXKNVRSGBLSVGVVRVKF 174
Db 121 SKTSAGLGLVGTGSYAVTPNVLDLADAGRYNYIGKVTXKNVRSGBLSVGVVRVKF 174

RESULT 8
US-10-467-657-2512

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; Sequence 2512, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2512
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2512

Query Match 93.3%; Score 809.5; DB 6; Length 175;
Best Local Similarity 93.1%; Pred. No. 3.1e-73;
Matches 163; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS 119
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 120 PSQTSIGLVLTGVSAYVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVVKF 174
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 PSKTSAGLVLTGVSAYVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVVKF 175
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
US-10-984-376-14
; Sequence 14, Application US/10984376
; Publication No. US2005024436A1
; GENERAL INFORMATION:
; APPLICANT: GIULIANI, Marzia Monica
; APPLICANT: RAPPUOLI, Rino
; TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS
; FILE REFERENCE: 2300-1609.20
; CURRENT APPLICATION NUMBER: US/10/984,376
; CURRENT FILING DATE: 2004-11-09
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: PCT/IB00/00828
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: GB 9911692.3
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: GB 9919705.5
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: GB 0005730.7
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nepa
US-10-984-376-14

Query Match 90.5%; Score 785.5; DB 6; Length 173;
Best Local Similarity 93.1%; Pred. No. 7.3e-71;
Matches 162; Conservative 1; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 59
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 60 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS 119
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 SQTSIGLVLTGVSAYVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVVKF 174
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 120 SQKSIALGVLTAVSAYVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVVKF 173
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-10-467-657-5652
; Sequence 5652, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
```

; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 5652

; LENGTH: 232

; TYPE: PRP

; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-5652

Query Match 25.8%; Score 224; DB 6; Length 232;

Best Local Similarity 27.5%; Pred. No. 3.1e-15;

Matches 64; Conservative 30; Mismatches 53; Indels 86; Gaps 9;

Qy 27 VOADAHAH-----AKASSSLGSAKGF-----SPRISAGYRINDLRPAV 63

Db 1 VOADLAYAAERITHDPEPTGAKKDKKISTVSDYFRNIRTHSVHPRVSGYDFGWSRIA 60

Qy 64 DYTRYKNY-----KAPSTDFK-----LYSIGASAIYDPT 93

Db 61 DYARYRWNNKSYVNIKRVKENNGSGKKLTQDLKTENQENGTFHVVSSGLSAYDPT 120

Qy 94 QSPVKPYLGARSLN--RASVDL-----GGSDFS--QTS----- 124

Db 121 GSRFPYAGVRSYGVHVRHSIDSTKKTVDVTAPTSTDGAPTYNANPQTPYHQSDS 180

Qy 125 ---IGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 174

Db 181 IRRVGLGVAGVGDITPNTLTDAGYRYHNWGRLENT-FTKTHEASLGMYRF 232

RESULT 12

US-10-467-657-6238

; Sequence 6238, Application US/10467657

; Publication No. US20050260581A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON Spa

; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASIGNANI Vega

; APPLICANT: MONACI Elisabetta

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 6238

; LENGTH: 229

; TYPE: PRP

; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-6238

Query Match 25.2%; Score 218.5; DB 6; Length 229;

Best Local Similarity 27.8%; Pred. No. 1.1e-14;

Matches 64; Conservative 29; Mismatches 54; Indels 83; Gaps 8;

Qy 27 VOADAHAHA-----SSLSGAK-----GFSPRISAGYRINDLRPAVD 64

Db 1 VOADLAYAAERITHDPEPTGKDKKISTVSDYFRNIRTHSVHPRVSGYDFGWSRIA 60

Qy 65 YTRYKNY-----KAPS-----TDFKLYSIGASAIYDPTQ 94

Db 61 YARYRWNNKSYVNTKRVKENNGEKNVTQYLKAENQENGTFHVVSSGLSAYDVKLN 120

Qy 95 SPVKPYLGARSLN--RASVDL-----GGS-----DSFSQTS 124

Db 121 DKFKPYIGARVAYGHVRHSIDSTKKTTEFLTAAGDGGGAPTVYNNGSTQDAHQSDSIRR 180

Qy 125 IGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 174

Db 181 VGLGVAGVGDITPNTLTDAGYRYHNWGRLENT-FTKTHEASLGMYRF 229

RESULT 13

US-10-467-657-6038

; Sequence 6038, Application US/10467657

; Publication No. US20050260581A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON Spa

; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASIGNANI Vega

; APPLICANT: MONACI Elisabetta

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 6038

; LENGTH: 226

; TYPE: PRP

; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-6038

Query Match 25.1%; Score 218; DB 6; Length 226;

Best Local Similarity 28.1%; Pred. No. 1.2e-14;

Matches 59; Conservative 28; Mismatches 57; Indels 66; Gaps 7;

Qy 30 DAAHAKASSSLGSAKGF-----SPRISAGYRINDLRPAVDYTRYK--NYKAPSTDF 78

Db 18 DAGANQKKISTVSDYFKNIRTHSIHPRVSGYDFGWSRIAADYARYRWNNKYSVDI 77

Qy 79 K-----LYSIGASAIYDPTQSPVKPYLGARSLN--RASV 112

Db 78 KELENKQNKRDLTENQENGSHAVSSGLSAYDVKLNDFKPKFYIGARVAYGHVRHSI 137

Qy 113 DL-----GGS-----DSFSQTSIGLVLTGVSVAVTNPVLD 144

Db 138 DSTKKTTEFLTAAGDGGAPTVYNNGSTQDAHQSDSIRRVLGVLGVIAGIPDITPKLTLD 197

Qy 145 AGYRYNYIGKNTVKNVRSGLSVGVVRKF 174

Db 198 TGYRYHNWGRLENT-FTKTHEASLGMYRF 226

RESULT 14

US-10-467-657-8006

; Sequence 8006, Application US/10467657

; Publication No. US20050260581A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON Spa

; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASIGNANI Vega

; APPLICANT: MONACI Elisabetta

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 8006

; LENGTH: 281

```
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-8006

Query Match      24.7%; Score 214; DB 6; Length 281;
Best Local Similarity 25.4%; Pred. No. 4e-14;
Matches 65; Conservative 31; Mismatches 68; Indels 92; Gaps 8;

Qy 10 ALALPAALAEQ---ASGFYQADAHA-----KASSSLGS-----A 43
Db 27 SLFSSAARAAGEDHGGPYVQADLAYAYEHITRDYPDAAGANKKISTVSDYFNIR 86
Qy 44 KGFSFRISAGYRINDLRFADVTRYK-----NYKAPST 76
Db 87 RSVHPRLAFGDFGWRIAADYARYRKWNHNNKYSVNIKELGRNDNSASDSKHLN 146
Qy 77 DFK-----LYSIGASAIYDFTQSPVKPYLGARLSNR-----ASVDLGG 117
Db 147 EHONGTTFHAVSSLSGLSTVYDFRANDKPKPYIGRVAYGHVRHQVHSMKEK 206
Qy 118 DSFSQTSI-----GLGLTGVSYAVTPNVLDAGYRYNYIGKNTV 158
Db 207 DGSAKTSVPSEMPKPAYHENRRRLGFGAGVGDVAPGLTLDAGRYHYWGRLE 266
Qy 159 KNVRSGELSGVRVKF 174
Db 267 R-PKTHEASLGVRYP 281

RESULT 15
US-10-467-657-6726
; Sequence 6726, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6726
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6726

Query Match      24.4%; Score 212; DB 6; Length 278;
Best Local Similarity 25.2%; Pred. No. 6.1e-14;
Matches 65; Conservative 28; Mismatches 71; Indels 94; Gaps 8;

Qy 10 ALALPAALAEQ---ASGFYQADAHA-----KASSSLGSAGK----- 45
Db 22 SLFSSAARAAGEDHGGPYVQADLAYAYEHITRDYPDAAGANKKISTVSDYFNIR 81
Qy 46 -FSFRISAGYRINDLRFADVTRYK-----NYKAPSTD 77
Db 82 SIHPRVSGVDFGWRIAADYARYRKWNHNNKYSVNIKELERKNNKTFGGNQLN 141
Qy 78 FK-----LYSIGASAIYDFTQSPVKPYLGARLSNR----- 110
Db 142 EHONGTTFHAVSSLSGLSTVYDFRVNDKPKPYIGRVAYGHVRHGDISTKTK 201
Qy 111 -----SVDLGS-----DSFSQTSIGLGLTGVSYAVTPNVLDAGYRYNY 156
Db 202 GTKFTYYDDIDSGKNQNTYRQNRRLGFGAGVGDVAPGLTLDAGRYHYWGRLE 261
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Qy 157 TVKNVRSGELSGVRVKF 174
Db 262 NTR-FKTHEASLGVRYP 278
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Search completed: January 11, 2006, 15:30:26
Job time : 30 secs